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   Claim 5; Page 18-19; 35pp;
                          Isolated gene encoding lactate dehydrogenase of and methods for diagnosis and vaccination again:
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N-PSDB; Q72947.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                 falciparum lactate dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAYYAPGASAIQMAESYLKDRKRVMVCSCYLQGQYGVQNHYLGVPCVIGGRGVEKIIELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GMVIGVHGDHMVPLSRYATVNGIPLSEFÝKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YCPNAFVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTGITYYGSNSYECLKGADYVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKS. 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gmvlgvhgdhmvplsryatvngiplsefvkkgwikgeevddivqktkvaggeivrllggg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTAGERGELGGSIDEVKEMOKAIAALDASK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sayyapgasaiqmaesylkdrkrvmvcscylqgqygvqnhylgvpcviggrgvekiiele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt ycpnafvinitnpldvmvaalqessglphhricgmagmldssrfrrmiadklevsprdvq}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acids (see also T51370).
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                                                                                                                                                                 1.94WO-US03796
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                             .93US-0046160
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                                                                                                                                                                                                                                                                serum; malaria
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99.7%;
                                                                                                                                                                                                                                                                           LDH;
                                                                                                                                                                                                                                                                                                                                                                        315
    English
                                                                                                                                                                                                                                                                         immunogen; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1685; DB 18; Pred. No. 2.5e-160;
                                                                                                                                                                                                                                                                                                                                                                        Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Live viral vaccines can also be
                         against malaria
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Best Local
    New antibodies to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents P. falciparum lactate dehydrogenase (LDH). The LDH protein and immunogenic fragments of it may be used as an immunogen for antibody generation. The progress of immunisation can be monitored by detection of antibody titres in plasma or serum. Antibodies raised against fragments of LDH can be used to immunise against P. falciparum infection and to detect early malarial
                              N-PSDB; X26909
                                         WPI; 1999-229405/19
                                                                   Bzik DJ,
                                                                                                                                                08-SEP-1998;
                                                                                                                                                                                                                            Plasmodium falciparum
                                                                                                                                                                                                                                                                                               A Plasmodium
                                                                                                                                                                                                                                                                                                                                                     Y01690;
                                                                                                                      17-SEP-1997;
                                                                                                                                                                          25-MAR-1999
                                                                                                                                                                                                                                                     Lactate dehydrogenase; LDH; antibody; antigenic peptide; malaria; immunization; Plasmodium falciparum infection.
                                                                                                                                                                                                                                                                                                                         23-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                           Y01690 standard; Protein;
                                                                                                                                                                                                   709913903-A1
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                                                                                            (DART-) DARTMOUTH COLLEGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 SAIQMAESYLKDRKRYMYCSCYLQGQYGVQNHYLGVPCVIGGRGVEKIIELELTAQERQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 sntyddlagadvvivtagftkapgksdkewnrddllplnnkimieigghikkncpnafii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 RPKIAMVGSGMIGGTMAFLCSLRELGDVVLFDVVPNMPMGKAMDISHNSSVVDTGITVYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DHMVPLSRYATVNGIPLSEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYYAPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQGSIDEVKEMQ 320
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                                                                   Fox
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                                                                                                                                                                                                                                                                                           falciparum lactate dehydrogenase
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                     97US-0932194.
                                                                                                                                               98WO-US18626
  Plasmodium
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falciparum
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 828; DB 15;
Pred. No. 1.1e-74;
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RESULT
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Best Local
                                                                                                                                                                               Misc-difference
WPI; 1996-166248/17
                                                     03-JUN-1994;
02-JUL-1993;
                                                                                           01-JUL-1994;
                                                                                                                     20-FEB-1996.
                                                                                                                                                JP08047389-A
                                                                                                                                                                                                                           Bacillus stearothermophilus
                                                                                                                                                                                                                                                  alpha-ketoglutaric acid; glutamine oxalo-transaminase
                                                                                                                                                                                                                                                                                          Heat resistant maleate dehydrogenase
                                                                                                                                                                                                                                                                                                                      21-AUG-1996
                                                                                                                                                                                                                                                                                                                                                R94013
                                                                                                                                                                                                                                                                                                                                                                         R94013 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dehydrogenase (LDH). The specification describes an antibody which binds to antigenic peptides derived from the LDH protein. The antibody can be used for diagnosing or treating malaria in a subject. The peptides and portions can be used for immunizing an individual against malaria and the antibody can also be used for diagnosing Plasmodium falciparum infectiv
                           (TOYM ) TOYOBO KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ø
                                                                                                                                                                                                                                                 resistant maleate dehydrogenase; h-rMAD; NADH; L-aspartic acid; a-ketoqlutaric acid; glutamine oxalo-transaminase activity; GOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHMVPLSRYATVNGIPLSEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYYAPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVIGVHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vvtnpvdvmvqllhqhsgvpknkiiglggvldtsrlkyyisqklnvcprdvnahivgahg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents a Plasmodium falciparum lactate
                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                   94JP-0121629.
93JP-0164701.
                                                                                         94JP-0151045
                                                                                                                                                                                     Location/Qualifiers
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52.6%;
                                                                                                                                                                      "Given in the specification
                                                                                                                                                                                                                                                                                                                                                                          329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                           ATCC 12016
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Pred. No. 1.1e-74;
1; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Q-PSDB; Bacillus sp.

Q10162

pref.

TP-262 stain

ST

thermophilic bacterium

WPI; 1991-012213/02 (TOYA) TOYAMA CHEM 27-APR-1989; 26-NOV-1990

89JP-0108432

89ЛР-0108432

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RESULT
R10591
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Best Local Sin
Matches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dehydrogenase (h-rMAD) activity. The protein has a residual activity after storage at 40 deg.C for 10 days of at least 60%, pref. 70% and esp. 90%. A reagent containing the h-rMAD protein, NADH and L-aspartic and alpha-ketoglutaric acid may be used for the determination of glutamine oxalo-transaminase (GOT) activity. The h-rMAD protein may be produced by transforming E. coli with the DNA encoding this protein and isolating the protein from the culture medium.
                                                                                                                                                                                     Bacillus strain
                                                                                                                                                                                                                                         L-lactic acid dehyrogenase
                                                                                                                                                                                                                                                                        20-MAR-1991
                                                                                                                                                                                                                                                                                                                             R10591 standard; Protein; 319
                                                                                                                                                        JP02286077-A
                                                                                                                                                                                                              LDH; L-lactic acid; thermophile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein having heat resistant maleate dehydrogenase activity - and reagent contg. protein, NADH and L-aspartic and alpha-keto:glutaric acid for determination of glutamine oxalo-transaminase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a protein having heat resistant maleate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Page 13-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GASAIQMAESYLKDRKRVMVCSCYLQGQYGVQNHYLGVPCVIGGRGVEKIIELELTAQER
                                                                                                                                                                                                                                                                                                                                                                                                 aaslvemveailkdqrrilpalaylegeygyegiylgvptilggngiekvielelteeek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGDHMVPLSRYATVNGIPLSEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYYAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               {\tt iivltnpvdamtytvfkesgfpknrviggsgvldtarfrtfvaeelnisvkdvtgfvlgg}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                     hgddmvplvrysyaggipleklipk----drldaivertrkgggeivnllgngsayyap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     igtsdyadtadsdivvitagiarkpg-----msrddlvttnqkimkqvtkevvkyspncy 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rkkisvigagftgattafllaqkelgdvvlvdipqlenptkgkaldmleaspvlgfdani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329
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                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                    TP-262
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45.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 706; DB 17;
Pred. No. 1.9e-62;
                                                                                                                                                                                                                                                                                                                             ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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RESULT
P91948
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                     Misc-difference
                                                                                                                                      Misc-difference
               17-MAR-1988;
                                                                                                                                                               Binding-site
                                                                                                                                                                                                                            Suidae.
                                                                                                                                                                                                                                             NAD-dependent lactate dehydrogenase;
                                                                                                                                                                                                                                                                                                                      P91948;
                                                                                                                                                                                                                                                                                                                                       P91948 standard; protein; 333 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence was deduced from DNA which can be used to produce L-LDH by recombinant DNA techniques. The bacillus species contg. the DNA and able to express it is new and is thermophilic, growing at 50-70 deg.C.
                                      16-MAR-1989;
                                                            21-SEP-1989
                                                                                   W08908707-A
                                                                                                                                                                                       Binding-site
                                                                                                                                                                                                                                                                        Pig H4 isoenzyme
                                                                                                                                                                                                                                                                                               16-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 16pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   producing L-lactic
                                                                                                                                                                                                                                                                                                                                                                                                     299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 KIAMVGSGMIGGTMAFLCSLRELGD-VVLFDVVPNMPMGKAMDISHNSSVVDTGITVYGS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMRE-VGAAIKSYCPNAFVI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rvaligtefvgasyafalmnggiadelvlidvnkekaegdvmdlnhgkvfapkpmniwhg
                                                                                                                                                                                                                                                                                                                                                                                                     qfhhsvtvlkdi 310
                                                                                                                                                                                                                                                                                                                                                                                                                         ELQGSIDEVKEM 319
                                                                                                                                                                                                                                                                                                                                                                                                                                            ASAIQMAESYLKDRKRVMVCSCYLQGQYGVQNHYLGVPCVIGGRGVEKIIELELTAQERQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dtelpvwshaeigsvpieqilsqndryrkedlenifvnvrdaayqvie--kkgatyygia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHMVPLSRYATVNGIPLSEFVKKG-WIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYYAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \hbox{-atnpvdiltyatw} kfsglpkervigsgtild tarfrflvseyfqvaptnvhayiigehg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dyqdc-qdadlvvicaganqkpge-----trldlvnknmnifktivdsvmksgfdgiflv 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
               88GB-0006358
                                     89WO-GB00279
                                                                                                                                                                  /note="substrate recognition site."
167..173
                                                                                                                                                                                       Location/Qualifiers 98..110
                                                                                                                                           /note="activator site."
102..102
                                                                                                       /note="basic AA."
                                                                                                                              'note="basic AA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 421; DB 12;
Pred. No. 5.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 125;
                                                                                                                                                                                                                                                H4
                                                                                                                                                                                                                                              isoenzyme
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RESULT
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Best Local Similarity
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                                                                                                                         Testis-specific lactate dehydrogenase; vaccine; female fertility
30-NOV-1987;
                                 08-JUN-1988
                                                                EP270056-A.
                                                                                                 synthetic
                                                                                                                                                              Testis-specific lactate dehydrogenase subunit LDH-C4.
                                                                                                                                                                                                    29-NOV-1990
                                                                                                                                                                                                                                                                   P80891 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence codes for the H4 isoenzyme of pig - an NAD-dependent lactate dehydrogenase. It is used to construct a recombinant enzyme in which AA102 and AA173 are basic, esp. Arg, and Gln resp. The mutation of AA102 results in the creation of a malate dehydrogenase from the lactate dehydrogenase framework, the mutation being on the mobile coenzyme loop and changing the substrate binding specificity of the protein. The mutation of AA173, which is in the activation site, decreases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant NAD-dependent and oxaloacetate, and has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sensitivity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; page 4.-5; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1989-292522/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                        230
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                                                                                                                                                                                                                                                                                                                                                 296 nargltsvinqklkddevaqlknsadtlwgiqkdlkdl 333
                                                                                                                                                                                                                                                                                                                                                                                   289 GGRGVEKIIELELTAQERQELQGSIDEVKEMQKAIAAL
                                                                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 schgwilgehgdssvavwsgvnvagvslqqlnpemgtdndsenw---kevhkmvvesay-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 ivkyspnciiivvsnpvdiltyvtwklsglpkhrvigsgcnldsarfrylmaeklgvhps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYBR-) UNIVERSITY OF BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 lflqtp-kivankdysvtanskivvvtagvrqqege----srlnlvqrnvnvfkfiipq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 gettipnnkitvvgvgqvg----macaisilgksltdelalvdvledklkgemmdlghgs
                                                                                                                                                                                                                                                                                                                                                                                                                --evikl--kgytnwaiglsvadliesmlknlsrihpvstmvggmygienevflslpcvl
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGEIVRLLGQGSAYYAPGASAIQMAESYLKDRKRVMVCSCYLQGQYGVQNH-YLGVPCVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVQGMVIGVHGDHMVPLSRYATVNGIPLSEF-----VKKGWIKQEEVDDIVQKTKVA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKNTRP--KIAMVGSGMIGGTMAFLCSLRELG----DVVLFDVVPNMPMGKAMDISHNS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                   (first entry)
87EP-0117688
                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dehydrogenase - which interconverts malate low dependence on fructose-1,6-biphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Atkinson
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Pred. No. 4.7e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                 B. burgdorferi antigenic protein, f874.aa
                                                                                                                     19-JUL-1999
                                                                                                                                       Y20054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This testis-specific lactate dehydrogenase sub-unit (LDH-C4) or one or more antigenic regions can be used in a vaccine prepn. to reduce female fertility. Larger peptides (or fusion proteins) are antigenic and smaller peptides become so when coupled to e.g. tetanus toxold.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA encoding sub-unit of testis lactate hydrogenase expressing antigenic polypeptide useful in vaccines for reducing female fertility.
                                             W09859071-A1
                                                             Borrelia burgdorferi
                                                                                 Antigenic
                                                                                                                                                        Y20054 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
          18-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; ; pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1988-156290/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOUN ) NORTHWESTERN UNIV.
                                                                                                                                                                                                                     295
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12-JUN-1987;
                                                                                                                                                                                                  302 dvvkinlnseeealfkksaetlwnigk 328
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                                                                                                                                                                                                                                                                                                                           NAFVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMV
                                                                                                                                                                                                                                                                                                                                               kvtsgkd-ysvsansrivivtagarqqege----trlalvqrnvaimkiiipaivhysp
                                                                                                                                                                                                                                   lkgyts--waiglsvmdlvgsilknlrrvhpvstmvkglygikeelflsipcvlgrngvs
                                                                                                                                                                                                                                                LLGQGSAYYAPGASAIQMAESYLKDRKRVMVCSCYLQGQYGVQNH-YLGVPCVIGGRGVE
                                                                                                                                                                                                                                                                                                                                                                                 \tt densqckitivgtgavgmacaisillkdladelalvdvaldklkgemmdlqhgslffsts
                                                                                                                                                                                                                    KIIELELTAQERQELQGSIDEVKEMQK 321
                                                                                                                                                                                                                                                                         igehgdssvplwsgvnvagvalktldpklgtdsdkehw-
                                                                                                                                                                                                                                                                                         IGVHGDHMVPLSRYATVNGIPL------SEFVKKGWIKQEEVDDIVQKTKVAGGEIVR 235
                                                                                                                                                                                                                                                                                                           dckilvvsnpvdiltyivwkisglpvtrvigsgcnldsarfryligeklgvhptschgwi
                                                                                                                                                                                                                                                                                                                                                         ITVYGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCP 123
                                                                                                                                                                                                                                                                                                                                                                                                    EKNTRPKIAMVGSGMIGGTMAFLCSLRELGD-VVLFDVVPNMPMGKAMDISHNSSVVDTG 63
                                                                                                                                                                                                                                                                                                                                                                                                                         101;
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                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                    first
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         98WO-US12718
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87US-0936451
                                                                                                                                                        Protein; 316
                                                                                                                  entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                23.9%;
                                                                               Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 403; DB 9;
Pred. No. 3.7e-32;
                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                               disease;
                                                                               infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 332;
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                                                                               detection
                                                                                                                                                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                      294
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                                                                                                        RESULT
Y25997
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B. flavum 18-OCT-1999

Y25997

standard;

Protein; 314

ΑA

9

Brevibacterium

Lactate dehydrogenase; destruction; lactic acid

lactate dehydrogenase protein.

(first entry)

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Query Match
Best Local
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention, which is suitable for use in a vaccine. The Bb polypeptide can be used in vaccines for eliciting protective antibodies to member the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can be used for detection of members of the Borrelia genus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a Borrelia burgdorferi (Bb) protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Borrelia burgdorferi nucleic acids - us products for the diagnosis, prevention and treatment caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-189980/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choi GH,
   292
                                                                          232
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                                                                                                                                                                                                                                                                                                                                                                                                                      11 KIAMVGSGMIGGTMAFLCSLRE--LGDVVLEDVVPNMPMGKAMDISHNSSVVDTGITV-Y 67
                                                                                                                                                                                                                                                                                                                                                                                        σ
                                                                                                                                                                                                                         vvasnpvdimtyvtmkyskfpihkvigtgtildtsrlryflsdhfnvntqnihsyimgeh 178
                                                                                                                                                                                                                                                                                                  g--tykdcanadivvitaglnqkpge----trldlvdknskifkdiltnvvssgfdgif 118
                                                                                                                                                                                                                                                                                                                                                                               ispkeldkfnssanqlk 308
                                     LTAQERQELQGSIDEVK 317
                                                                       yyaiglgiknivnaiigdqnvilpissyingqygglikdiyigapaivckegvkevlnik
                                                                                                    YYAPGASAIQMAESYLKDRKRVMVCSCYLQGQYG--VQNHYLGVPCVIGGRGVEKIIELE 300
                                                                                                                                                xd-----ssfatwdetkiamkplseylaegkiteleldeihkkvvnaayevikl--kgat
                                                                                                                                                                     GDHMYPLSRYAT-----VNGIPLSEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQGSA 242
                                                                                                                                                                                                                                                              INITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVIGVH 187
                                                                                                                                                                                                                                                                                                                           GSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAFV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                              87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIMMUNE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316
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97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 398; DB 20;
Pred. No. 1.1e-31;
89; Mismatches 117
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diseases
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RESULT 10
R15736
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA with the lactate dehydrogenase gene on the chromosome DNA of the microbe cell and a method for the preparation of an amino acid or an organic acid in which the above strain destroying the lactate dehydrogenase gene is cultured in a medium and the amino acid or the cromation of lactic acid in the preparation of an amino acid and an organic acid can be decreased with no control of oxygen concentration during culture. This sequence represents the lactate dehydrogenase protein described in the specification.
                            17-MAR-1992
                                                                R15736;
                                                                                              R15736 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 11-12; 13pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes the isolation of a novel lactate dehydrogenase protein from Brevibacterium flavum strain MJ-233. The invention also describes a microbial strain destroying the lactate dehydrogenase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New lactate dehydrogenase gene and strain destroying gene - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a microbe in which the lactate dehydrogenase gene is destroyed by a nomologous recombination of the above DNA or the above recombinant vector DNA with the lactate dehydrogenase gene on the chromosome DNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MITU ) MITSUBISHI CHEM CORP
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                                                                                                                                                                                                                                                                                                                              181 dtelpvlssatiagvslsrmldkdpelegrlekifedtrdaayhiid--akgstsygigm
                                                                                                                                                                                      299 fkhsantlreigk 311
                                                                                                                                                                                                                                                        239 glaritrahlqnqdvavpvsallhgeygeediyigtpavvnrrgirrvveleitdhemer 298
                                                                                                                                                                                                                                                                                                                                                                                                             122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 KIAMVGSGMIGGTMAFLCSLRELGD-VVLFDVVPNMPMGKAMDISHNSSVVDTGITVYGS 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMRE-VGAAIKSYCPNAFVI 128
                                                                                                                                                                                                                                                                                        SAIQMAESYLKDRKRVMVCSCYLQGQYGVQNHYLGVPCVIGGRGVEKIIELELTAQERQE 308
                                                                                                                                                                                                                                                                                                                                                                  DHMVPLSRYATVNGIPLSEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYYAPGA 248
                                                                                                                                                                                                                                                                                                                                                                                                    -asnpvdiltyavwkfsglewnrvigsgtvldsarfrymlgelyevapssvhayiigehg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyadc-edaamvvicagaagkpge-----trlqlvdknvkimksivgdvmasgfdgiflv 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kivligagdvgvayayalinqgmadhlaiididekklegnvmdlnhgvvwadsrtrvtkg 67
                                                                                                                                                                                                                            LQGSIDEVKEMQK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                          (first entry)
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                                                                                              Protein; 328 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 397.5; DB 20; Pred. No. 1.2e-31;
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RESULT 11
W33107
ID W33107
XX
XX
W33107
XX
DT 28-JAN
XX
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DE Chicke
XX
KW Chicke
KW CLDH-B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
      Chicken;
cLDH-B4 i
                                            Chicken lactic acid dehydrogenase type B subunit.
                                                                                                                  W33107;
                                                                                                                                           W33107 standard; Protein; 333 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of a new L-lactic acid dehydrogenase which may produced in large amts. The enzyme can produce lactic acid in vitro from pyruvic acid and may be produced directly by culturing a transformed bacteria in which the gene is introduced.
                                                                                  28-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New L-lactic acid dehydrogenase and gene encoding it - for producing L-lactic acid in vitro in high yield from pyruvic
                                                                                                                                                                                                                                                                                                                                                       178
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                                                                                                                                                                                                                             296
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                                                                                                                                                                                                                                                       303 AQERQELQGSIDEVK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                          124 NAFVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMV, 183
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                                                                                                                                                                                                                          daeqqkmkasadelq 310
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                                                                                                                                                                                                                                                                                                                                               mgehgdsefavwshaniagvnleeflkdkenvqeaelvelfegvrdaaytiin--kkgat 235
                                                                                                                                                                                                                                                                                yygiavalaritkailddenavlplsvfqegqygvnnifigqpaivgahgivrpvnipln 295
                                                                                                                                                                                                                                                                                                                                                                  IGVHGDHMVPLSRYATVNGIPLSEFVK-KGWIKQEEVDDIVOKTKVAGGEIVRLLGQGSA 242
                                                                                                                                                                                                                                                                                                                                                                                                           ngiflvaanpvdvltystwkfsgfpkervigsgtsldsarfrqalaeklnvdarsvhayi 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pkkiyaakyedcadadlvvitagapqkpge----trldlvgknlainksivtqvvesgf 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITVYGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kvilvgdgavgssyafalvnqgiaqelgii----eipqlfekavgdaldlsh--alpfts 62
lactic acid dehydrogenase; LDH;
isozyme; reagent; transaminase; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 AA;
                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 391.5; DB 1
Pred. No. 5.2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                type B subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12;
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                tetramer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328;
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determination

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 97
 Gallus
                       Chicken; lactic acid dehydrogenase; LDH; cLDH-B4 isozyme; reagent; transaminase;
                                                           Chicken lactic acid dehydrogenase type B subunit.
                                                                                           28-JAN-1998
                                                                                                                     W33108
                                                                                                                                             W33108 standard; Protein; 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding chicken lactic acid dehydrogenase type B subunit - which can form tetramer, useful as reagent for transaminase activity determination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is chicken lactic acid dehydrogenase (LDH) type B subunit, which can form a tetramer to give of isozyme. The CLDH-84 isozyme can be used as a reagent for transaminase activity determination.
                                                                                                                                                                                                                 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Pages 9-10; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; T88365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-544152/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-0CT-1997.
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                                                                                                                                                                                                                                           303
                                                                                                                                                                                                                                                                                      244 YAPGASAIQMAESYLKDRKRVMVCSCYLQGQYGVQNH-YLGVPCVIGGRGVEKIIELELT 302
                                                                                                                                                                                                                                                                                                                192 ehgdssvavwsgvnvvgvslqelnpamgtdkdsenwkevhkqvvesayevirl--kgytn
                                                                                                                                                                                                                                                                                                                                         186 VHGDHMVPLSRYATVNGIPLSEF-VKKGWIKQEEVDDIVQKTKVAGG-EIVRLLGQGSAY 243
                                                                                                                                                                                                                                                                                                                                                                     132 tilvvsnpvdiltyvtwklsglpkhrvigsgcnldtarfrylmaerlgihptschgwilg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ORIY ) ORIENTAL YEAST CO LTD
                                                                                                                                                                                                                                                                     250
                                                                                                                                                                                                                                                                                                                                                                                                        126
                                                                                                                                                                                                                                                                                                                                                                                                                          77 ivadkdyavtanskivvvtagvrqqege----srlnlvqrnvnvfkfiipqivkyspnc
                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11
                                                                                                                                                                                                                                                             waiglsvaelcetmlknlyrvhsvstlvkgtygiendvflslpcvlsasgltsvingklk 309
                                                                                                                                                                                                             ddevaglkksadtlwsigkdlkdl 333
                                                                                                                                                                                                                                                                                                                                                                                              FVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VYGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kitvvgvgqvg----macaisilgkglcdelalvdvledklkgemmdlqhgslflqth-k 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIAMVGSGMIGGTMAFLCSLRELG-----DVVI.FDVVPNMPMGKAMDISHNSSVVDTGIT
                                                                                                                                                                                                                                       AQERQELQGSIDEVKEMQKATAAL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity
97; Conserv
domesticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 AA;
                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.2%; Score 391; DB 1
29.9%; Pred. No. 6e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69; Mismatches 138;
                                                                                                                                             Ş
                       determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 18; Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cLDH-B4
                                    tetramer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  185
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Y20055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                            B. burgdorferi antigenic protein, t874.aa
                                                                    Antigenic protein;
                                                                                                                       19-JUL-1999
                                                                                                                                                Y20055
                                                                                                                                                                       Y20055 standard; Protein;
                                            Borrelia burgdorferį.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is chicken lactic acid dehydrogenase (LDH) type B subunit, which can form a tetramer to give cLDH-B4 isozyme can be used as a reagent for transaminase activity determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Pages 10-11; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding chicken lactic which can form tetramer, use
                                                                                                                                                                                                                                                                                                                                        192
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                                                                                                                                                                                                                                                                                                                                                                                  132 vilvvsnpvdiltyvtwklsglpkhrvigsgcnldtarfrylmaerlgihptschgwilg
                                                                                                                                                                                                                                   310 ddevaqlkksadtlwsiqkdlkdl 333
                                                                                                                                                                                                                                                             303 AQERQELQGSIDEVKEMQKAIAAL 326
                                                                                                                                                                                                                                                                                                                                                                                                 126 FVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVIG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                           77
                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 VYGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 KIAMVGSGMIGGTMAFLCSLRELG-----DVVLFDVVPNMPMGKAMDISHNSSVVDTGIT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 kitvvgvgqvg----macaisilgkglcdelalvdvledklkgemmdlqhgslflqth-k 76
                                                                                                                                                                                                                                                                                ehgdssvavwsgvnvagvslqqldpamgtdkdsenwkevhkqvvesayevirl--kgytn
                                                                                                                                                                                                                                                                                                                                                                                                                                   ivadkdyavtanskivvvtagvrqqege----srlnIvqrnvnvfkfiipqivkyspnc 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333 AA;
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                                                                                                                    (first entry)
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                                                                      vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.1%; Score 390; DB 18; 29.6%; Pred. No. 7.5e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tic acid dehydrogenase type B subunit - useful as reagent for transaminase act
                                                                                                                                                                       295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70; Mismatches
                                                                   Lyme disease; infection;
                                                                                                                                                                       ĄΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                   detection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity
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RESULT
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Best Local S
Matches '82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can a
haematopolesis regulator; tissue growth regulator; tumour inhibitor; penetic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Borrelia burgdorferi nucleic acids - us products for the diagnosis, prevention and treatment caused by Borrelia, particularly Lyme disease
                                                                                Extended human secreted protein sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-189980/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choi GH,
                                                                                                                                                                  Y36058 standard; Protein; 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Page 177; 275pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-1997;
22-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-1998;
                                                                                                                                                                                                                                       237 syingqygglikdiyigapaivckegvkevlnfkispkeldkfnssanglk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity es '82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used for
                                                                                                                                                                                                                                                                 CYLQGQYG---VQNHYLGVPCVIGGRGVEKIIELELTAQERQELQGSIDEVK 317
                                                                                                                                                                                                                                                                                                                        VKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYYAPGASAIQMAESYLKDRKRVMVCS 268
                                                                                                                                                                                                                                                                                                                                                                               GMAGMLDSSRFRRMIADKLEVSPRDVQGMVIGVHGDHMVPLSRYAT-----VNGIPLSEF
                                                                                                                                                                                                                                                                                                                                                                                                                                       SDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAFVINITNPLDVMVAALQESSGLPHHRIC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 elviidvnenkakgevmdlnhgqmflkkninvlfg--tykdcanadivvitaglngkpge 68
                                                                                                                                                                                                                                                                                            laegkiteleldeihkkvvnaayevikl--kgatyyaiglgiknivnaiigdqnvilpis
                                                                                                                                                                                                                                                                                                                                                  gtgtildtsrlryflsdhfnvntqnihsyimgehxd----ssfatwdetkiamkplsey
                                                                                                                                                                                                                                                                                                                                                                                                           -----trldlvdknskifkdiitnvvssgfdgifvvasnpvdimtyvtmkyskfpihkvi 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection of members of the Borrelia genus.
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                                                                                                             (first entry)
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97US-0053344.
97US-0053377.
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28.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 371; DB 20,
Pred. No. 5e-29;
""smatches 108;
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                                                                                  SEQ ID NO.
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nt of diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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17-DEC-1997;
09-FEB-1998;
13-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression the genes corresponding to the extended cDNAS. They are also useful for constructing a high resolution map of the human chromosomes. They can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of the invention. The secreted proteins can be used in treating or controlling a variety of human conditions. The secreted proteins may act as cytokines or may affect cellular prollieration or differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is encoded by an extended human secreted protein coding sequence of the invention. The secreted proteins can be used in treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth regulators, regulators of reproductive hormones or or have chemotactic/chemokinetic, receptor/ligand, anti-ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-385906/32
N-PSDB; X97742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or may act as immune system regulators, haematopoiesis regulators, tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 379-381; 516pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human secreted proteins
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                                                                                                                                                                                                                                   130 ITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVIGVHGD 189
                                                                                                                                                                                                                                                                    130 kxyfvtansnlviitagarqxkge-----trlnlxqrnvaifklmissivqysphcklii 184
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                                                                                                                                                                                                                                                                                                                                                                            11 KIAMVGSGMIGGTMAFLCSLRELGD-VVLFDVVPNMPMGKAMDISHNSSVVDTGITVYGS
                                                                                                                               ssvpvwsgvniagvplkdlnsdigtdkdpegwknvhkevtatayeiikmkgyts--waig
                              QELQGSIDEVKEMQKAI
                                                            ASAIQMAESYLKDRKRVMVCSCYLQGQYGV-QNHYLGVPCVIGGRGVEKIIELELTAQER
                                                                                                                                                                                                 vsnpvdilty vawkls af pknriigs gcnlix arfrfliggklgihses chgwilgehgd\\
                                                                                                                                                                                                                                                                                                       NSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAFVIN 129
                                                                                                                                                                                                                                                                                                                                      kvsiigtgsvgmacaisillkglsdelalvdldexklkgetmdlqhgspftkmp-nivcs 129
                                                                                                                                                                                                                                                                                                                                                                                                                 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for gene therapy to control or treat
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97US-0069957.
98US-0074121.
98US-0081563.
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                                                                                                                                                                                                                                                                                                                                                                                                                                21.1%;
28.1%;
                              323
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 356; DB 20; Pred. No. 2.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor/ligand, anti-inflammatory or
                                                                                                                                                                                                                                                                                                                                                                                                               143;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      procedures
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302 247 244 69

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Query Match 20.9
Best Local Similarity 25.6
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This recombinant thermophilic NAD-dependant dehydrogenase has a sequence with at least 75% homology with that of B.Stearothermophilus lactate dehydrogenase. The altered amino acids are at posns. 106-110 and 167-172. It has a higher catalytic activity for homologues of lactic acid of formula: C(n) H(2n + 1) CHORCOH, n= greater than 1, than for lactate as well as a higher catalytic activity for malate than for lactate. It can be used to convert a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              keto cpd. stereospecifically to a corresp. This prodn. of individual optical isomers mfr. of o.i.'s of pharmaceuticals and drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant thermophilic NAD-dependent dehydrogenase - having a hydrophobic amino acid at position 102 and/or 104 and/or a change at 234-237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; fig 1; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chia WN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified dehydrogenases; keto compounds; secondary alcohols; optical isomers; pharmaceuticals; drug intermediates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant thermophilic NAD-dependant dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PUBL-) PUBLIC HEALTH LAB S. (UYBR-) UNIV BRISTOL.
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                                             184 IGVHGDHMVPLSRYATVNGIPLSEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQGSAY 243
                                                                                                           116
                                                                                                                            124 NAFVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMV 183
            176
                                                                                                                                                                                               64 ITVYGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCP 123
                                                                                                                                                                                                                                                                                                knnggarvvvigagfvgasyvfalmnggiadeivlidaneskaigdamdfnhgkvfapkp 61
                                                                                              qqlflvatnpvdiltyatwkfsglphervigsgtildtarfrfllgeyfsvldxarfayi 175
                                                                                                                                                                                                                                                                                                                                             EKNTRPKKAMVGSGMIGGTMAFLCSLRELGD-VVLFDVVPNMPMGKAMDISHNSSVVDTG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clarke AR,
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                                                                                                                                                                                                                                                                                                                                                                                                20.9%; Score 352.5; DB 11; Length 25.6%; Pred. No. 3.6e-27; tive 70; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Holbrook
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Wilks HM,
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Search completed: November 15, 2000, 09:48:27 Job time: 103 sec

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276 deknrfhhsaatlksv

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Result
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1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/2
3: /cgn2_6/ptodata/2
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Listing first 45 summaries
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US-07-642-734C-2

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                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 227-59
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
189 DHMVPLSRYATVNGIPLSEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYYAPGA 248
                                          124 VYTNPVDVMVQLLHQHSGVPKNKIIGLGGVLDTSRLKYYISQKLNVCPRDVNAHIVGAHG
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                                                                              129
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TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 12-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: DCI-066CPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 315 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
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                                                                     NITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVIGVHG
                                                                                                SNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAFVI 128
                                                                                                                                                        KAKIVLVGSGMIGGVMATLIVQKNLGDVVLFDIVKNMPHGKALDTSHTNVMAYSNCKVSG 63
                                                                                                                                                                                   RPKIAMVGSGMIGGTMAFLCSLRELGDVVLFDVVPNMPMGKAMDISHNSSVVDTGITVYG 68
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                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                               Score 828; DB 4;
Pred. No. 5.9e-83;
                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                     95;
                                                                                                                                                                                                                                              Length 315;
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Best Local
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                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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                              120 IIVLTNPVDAMTYTVFKESGFPKNRVIGQSGVLDTARFRTFVAEELNISVKDVTGFVLGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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187 HGDHMVPLSRYATVNGIPLSEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYYAP 246
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TELECOMMUNICATION INFORMATION:
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                                                                                                65 IGTSDYADTADSDIVVITAGIARKPG-----MSRDDLVTTNQKIMKQVTKEVVKYSPNCY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM FC DOS/MS-LUG
OPERATING SYSTEM: PC-DOS/MS-LUG
OPETWARE: Patentin Release #1.0, Version
                                                                                                                                           67
                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                              9 RPKIAMVGSGMIGGTMAFLCSLRELGDVVLFDV--VPNMPMGKAMDISHNSSVVDTGITV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Green, Robert
REGISTRATION NUMBER:
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                                                                                                                             YGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAF 126
                                                                                                                                                               RKKISVIGAGFTGATTAFLLAQKELGDVVLVDIPQLENPTKGKALDMLEASPVLGFDANI
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o. 5686294
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02-JUL-1993
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GENERAL INFORMATION:
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NFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
                                127 VINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVIGV 186
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                                                                                      67 YGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLÞVNIKIMREVGAAIKSYCPNAF 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hoover, Allen E. REGISTRATION NUMBER: 3
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                                                                                                                                                                 9 RPKIAMVGSGMIGGTMAFLCSLRELGDVVLFDV--VPNMPMGKAMDISHNSSVVDTGITV 66
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ZIP: 60601-6780
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OPERATING SYSTEM: PC-DOS/MS-DOS
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IIVLTNPVDAMTYTVFKESGFPKNRVIGQSGVLDTARFRTFVAEELNISVKDVTGFVLGG 179
                                                                IGTSDYADTADSDIVVITAGIARKPG-----MSRDDLVTTNQKIMKQVTKEVVKYSPNCY 119
                                                                                                                                 RKKISVIGAGFTGATTAFLLAQKELGDVVLVDIPQLENPTKGKALDMLEASPVLGFDANI 64
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Two Prudential Plaza, Suite 4900
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Pred. No. 1:7e-69;
4; Mismatches 88
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                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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PRIOR APPLICATION NUMBER: 08/256,959
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CURRENT APPLICATION DATA
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FILING DATE: 05-0CT-1994
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                                                                                                                                                         Modified-site (30~31)
                                                                              Modified-site (40^41)
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                      Modified-site (69^70)
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Modified-site

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; LOCATION: (286^28); OTHER INFORMATION: US-08-748-068-3
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                                                                     124 NAFVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMV 183
                                                                                                                                64 ITVYGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCP 123
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les 89; Conserv
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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                                                                                                 VDIWHGDYDDC-RDADLVVICAGANQKPGE-----TRLDLVDKNIAIFRSIVESVMASGF 115
IGVHGDHMVPLSRYATVNGIPLSEFVK-KGWIKQEEVDDIVQKTKVAGGEIVRLLGQGSA 242
                                                                                                                                                            KNNGGARYVVIGAGFVGASYVFALMNQGIADEIVLIDANESKAIGDAMDFNHGKVFAPKP 61
                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                             RAGMENT TYPE:
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STITUG DATE: 05-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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                                                                                       NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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; LOCATION: (302^30:); OTHER INFORMATION: US-08-748-068-1
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Best Local Similarity
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NAME/KEY:
184 SCHCWILGEHGDSSVAVWSGVNVAGVSLQQLNPEMGTDNDSENW---KEVHKMVVESAY- 239
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                                                                                                                                                                       14 QETTIPNNMITVVGVGQVG----MACAISILGKSLTDELALVDVLEDKLKGEMMDLQHGS
                                                                                                                                           58 SVVDTGITVYGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKINREVGAA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                               70 LFLQTP-KIVANKDYSVTANSKIVVVTAGVRQQEGE----SRLNLVQRNVNVFKFIIPQ 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site (245^246)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site (210~211)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (249~250)
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                                                                                                                                                                                                                                ; Score 412; DB 1;
; Pred. No. 4.2e-37;
73; Mismatches 130
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                             -VKKGWIKQEEVDDIVQKTKVA 229
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186 VHGDHMVPLSRYATVNGIPLSEF-VKKGWIKQEEVDDIVQKTKVAGG-EIVRLLGQGSAY 243

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MOLECULE TYPE:

US-08-869-506-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08869506 Patent No. 5827710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 29-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
132 TILVVSNPVDILTYVTWKLSGLPKHRVIGSGCNLDTARFRYLMAERLGIHPTSCHGWILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                            126 FVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVIG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 110.
CTTY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                          66 VYGSNSYECLKGADVVIITAGITKIPGKSDKENSRMDLLPVNIKIMREVGAAIKSYCPNA 125
                                                                                                                             77 IVADKDYAYTANSKIVVVTAGVRQQEGE-----SRLNLVQRNVNVFKFIIPQIVKYSPNC
                                                                                                                                                                                                                                                           22 KITVVGVGQVG----MACAISILGKGLCDELALVDVLEDKLKGEMMDLQHGSLFLQTH-K 76
                                                                                                                                                                                                                                                                                                                           11 KIAMVGSGMIGGTMAFLCSLRELG-----DVVLFDVVPNMPMGKAMDISHNSSVVDTGIT 65
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TE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 73797/1996 FILING DATE: 29-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 GGEIVRLLGOGSAYYAPGASAIQMAESYLKDRKRVMVCSCYLGGQYGVQNH-YLGVPCVI 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 05-JUL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 391; DB 2;
Pred. No. 8.7e-35;
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                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                             NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tent No. 6057
                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 29-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT: Fujita, Tuyosi
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                                                                                                11 KIAMVGSGMIGGTMAFLCSLRELG-----DVVLFDVVPNMPMGKAMDISHNSSVVDTGIT 65
                                                                                                                                                    Local
                                                                                                                                                                                                                                                TOPOLOGY:
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ZIP: 22201-4741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
              77 IVADKDYAVTANSKIVVVTAGVRQQEGE--
                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                             ENGTH:
                                                                     KITVVGVGQVG----MACAISILGKGLCDELALVDVLEDKLKGEMMDLQHGSLFLQTH-K 76
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1100 No. 6057141th Glebe Rd.
                                                                                                                                                                                                                                                                                                                     703-816-4100
                                                                                                                                     Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                  23.2%;
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                                                                                                                                                  Score 391; DB 3;
Pred. No. 8.7e-35;
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                                                                                                                                    Mismatches
           -- SRLNLVQRNVNVFKFIIPQIVKYSPNC 131
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                                                                                                                                    138;
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 05-JUN-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polania
                    11 KIAMVGSGMIGGTMAFLCSLRELG-----DVVLFDVVPNMPMGKAMDISHNSSVVDTGIT 65
22 KITYVGVGQVG----MACAISILGKGLCDELALVDVLEDKLKGEMMDLQHGSLFLQTH-K 76
                                                                                                                                                                                                     STRANDEDNESS
                                                                                       Local Similarity
                                                                                                                                                                                         TOPOLOGY:
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                                                                                   23.1%; 29.6%;
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                                                                                  Score 390; DB 2; Pred. No. 1.1e-34;
                                                                    Mismatches
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Query Match
Best Local Similarity
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                                                                                                                                                                                             NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                      MOLECULE TYPE:
                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                           TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                FILING DATE: 29-MAR-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                   STRANDEDNESS
                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                 REGISTRATION, NUMBER:
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                                                                                                                                                         ENGTH:
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DO NO. 6057141th Glebe Rd.
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29-MAR-1996
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23.1%; 29.6%;
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R: 159-43
Score 390; DB 3; Pred. No. 1.1e-34;
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                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                   FEATURE:
                                                                                                                                                 FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 WAIGLSVAELCETMLKNLYRVHSVSTLVKGTYGIENDVFLSLPCVLSASGLTSVINQKLK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 YAPGASAIQMAESYLKDRKRYMYCSCYLQGQYGYQNH-YLGVPCYIGGRGVEKIIELELT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 VHGDHMVPLSRYATVNGIPLSEF-VKKGWIKQEEVDDIVQKTKVAGG-EIVRLLGQGSAY 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 VILVVSNPVDILTYVTWKLSGLPKHRVIGSGCNLDTARFRYLMAERLGIHPTSCHGWILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 FVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVIG 185
                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 DDEVAQLKKSADTLWSTQKDLKDL 333
                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: GB 92 04702.6 FILING DATE: 04-MAR-1992
                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 05-OC
                                                                                               NAME/KEY: Modified-site LOCATION: (16^17)
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EHGDSSVAVWSGVNVAGVSLQQLDPAMGTDKDSENWKEVHKQVVESAYEVIRL--KGYTN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KITVVGVGQVG----MACAISILGKGLCDELALVDVLEDKLKGEMMDLQHGSLFLQTH-K 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIAMVGSGMIGGTMAFLCSLRELG-----DVVLFDVVPNMPMGKAMDISHNSSVVDTGIT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQERQELQGSIDEVKEMQKAIAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96;
          INFORMATION:
                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                     327 amino acids
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                            Modified-site (27^28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible YSTEM: PC-DOS/MS-DOS
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                                                                                                                                                internal
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   /note= "- numbering discontinuity"
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NAME/KEY:
LOCATION:
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OTHER INFORMATION: /note= "--- numbering
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LOCATION:
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OTHER INFORMATION:
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                                                                                                         OTHER INFORMATION:
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                                                                                                                      Modified-site (262~263)
                                                                                                                                                                                                                                                                                Modified-site (243^244)
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                                                                 Modified-site (275^276)
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Modified-site (298^299)
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RESULT 12
US-08-211-682-25
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                           Query Match
Best Local Similarity 24...
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application Patent No. 5670333
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Best Local :
                                                                                                                                                                                                                           APPLICATION NUMBER: UINFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 LTAQERQELQGSIDEVKEMQK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 --WAIGLSVMDLVP--LKNLRRVHPVSTMVKGLYGIKEELFLSIPCVLGRNGVSDVVKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 SSVPLWSGVNVAGVALKTLDPKLGTDSDKEHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 HMVPLSRYATVNGIPL------SEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQGS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 VSNPVDILTYIVWKISGLPVTRVIGSGCNLDSARFRYLIGEKLGVHPTSCHGWIIGEHGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 ITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVIGVHGD
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified LOCATION: (326~327 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 D-YSVSANSRIVIVTAGARQQEGE-----TRLALVQRNVAIMKIIIPAIVHYSPDCKILV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 NSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAFVIN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 KIAMVGSGMIGGTMAFLCSLRELGD-VVLFDVVPNMPMGKAMDISHNSSVVDTGITVYGS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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                                                                                                                                                                                            327 amino acids
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                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                               9.2%; Score 155; DB 1; 24.3%; Pred. No. 8.3e-09;
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31.2%;
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Pred. No. 2.6e-33;
                                                 Mismatches
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                                                                             Length 327;
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TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1994 TELEFAX: 415/952-9881 TELEX: 910/371.7168 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 814 amino acids TYPE: amino acid TOPOLOGY: linear US-08-286-305A-3	PILING DATE: 05-AGG-1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/170558 FILING DATE: 20-DEC-1993 PRIOR APPLICATION NUMBER: 08/170563 PRIOR APPLICATION ONATA: APPLICATION NUMBER: 08/157563 FILING DATE: 23-NOV-1993 ATTORNEY/AGENT INFORMATION: NAME: Lee-, Wendy M. REGISTRATION NUMBER: 00,000 REFERENCE/DOCKET NUMBER: 854C1P1	YESEQUENCES: 11 NDENCE ADDRESS: 2460 Point San Bruno Blvd South San Francisco California 24 USA 24 USA 27 USA TYPE: 5.25 inch, 360 Kb floppy disk TYPE: 5.25 inch, 360 Kb floppy disk TYPE: PC-DOS/MS-DOS RE ADDRESD: UFC/OS/MS-DOS REPAITON DATA: TON NUMBERD: UFC/OS/MS-DOS	RESULT 13 US-08-286-305A-3 ; Sequence 3, Application US/08286305A. ; Patent No. 5766863 ; Patent No. 5766863 ; GENERAL INFORMATION: ; APPLICANT: Godowski, Paul J. ; APPLICANT: Mark, Melanie R. ; APPLICANT: Sadick, Michael D. ; APPLICANT: Shelton, David L. ; APPLICANT: Wong, Wai Lee Tan ; TITLE OF INVENTION: KINASE RECEPTOR ACTIVATION ASSAY	QY 180 QGMVI-GVHGDHWVPLSRYATVNGIPLSEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLG 238 	62 66 122
- вывыны Бойфойфо	COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 720 kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patin (Geneatech) CURRENT APPLICATION NDATA: APPLICATION NUMBER: US/08/441,104A FILING DATE: 15-MAY-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/286305 FILING DATE: 05-AUG-1994 EPRIOR ADELICATION DATA: APPLICATION NUMBER: 08/286305	APPLICANT: GOOWSKI, Paul J. APPLICANT: GOOWSKI, Paul J. APPLICANT: Mark, Melanie R. APPLICANT: Sadick, Michael D. APPLICANT: Sadick, Michael D. APPLICANT: Solick, Michael D. APPLICANT: Wong, Wal Lee Tan TITLE OF INVENTION: KINASE RECEPTOR ACTIVATION ASSAY NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc. STREET: 460 Point San Bruno Blvd CITY: South San Francisco STATE: California COUNTRY: USA ZIP: 94080	9 ALRWLQRWEEEGLGGVPEQKLQCHGQGPLAHMPNASC		Query Match S.2%; Score 87; DB 1; Length 814; Best Local Similarity 20.1%; Pred. No. 1.1; Matches 71; Conservative 36; Mismatches 83; Indels 164; Gaps Oy 20 IGGTMAFICSLRELGDVVLFDVVPNMPMGKAMDISHNSSVVDTGITVYGSNSYECLKGAD 79 I

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Best Local Similarity
Thiches 71; Conserv.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE; 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: pdtin (Genentech)
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tent No. 59142
                                CLASSIFICALLO... DATA:
PRIOR APPLICATION NUMBER: 08/286305
APPLICATION NUMBER: 08/286305
APPLICATION NUMBER: 05-AUG-1994
                                                                                                                                                            SOFTWARE: patin (Genen CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 08/1
FILING DATE: 20-DEC-1993
                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 15-MAY-1995
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STATE: California
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460 Point San Bruno Blvd
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Shelton, David L.
Wong, Wai Lee Tan
WENTION: KINASE RECEPTOR ACTIVATION ASSAY
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20.1%; Pred. No.
                  08/170558
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Search completed: November 15, 2000, 09:47:18 Job time: 34 sec

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Matches 71; Conserv
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INFORMATION FOR SEQ ID NO:
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NAME: Lee, Wendy M.
        216
                                         267 CSCYLOGOYGVONHYLGVP----
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-GVPTLKVQVPNASVDVGDDVLLRCQVEGRGLEQAGWILTELEQSA 260
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20.1%; Pred. No.
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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1688
1 MAVFEKNTRPKIAMVGSGMI.....GSIDEVKEMQKAIAALDASK 330
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/cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:
                 /cgn2_6/ptodata/2/paa/US60_COMB.pep:*
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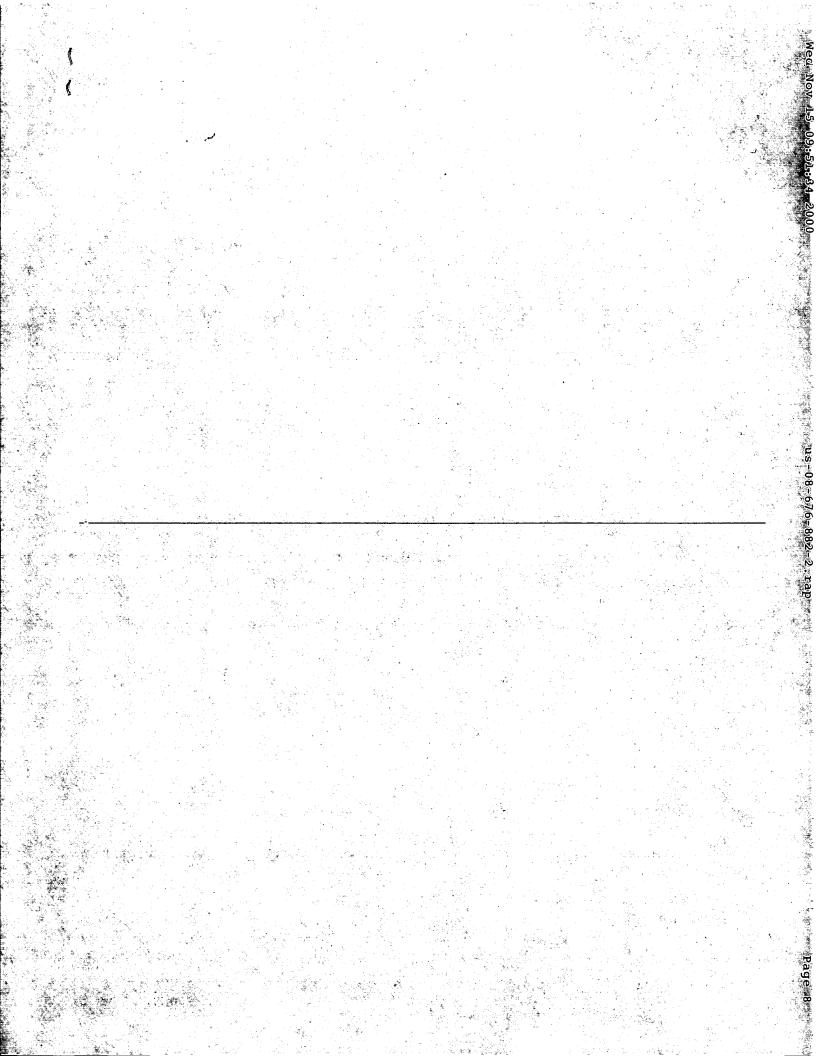
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB		ID	Description
1	828	49.1	315	ь ;	PCT-US98-18626-2	Sequence 2, Appli
2	828	49.1	315	4	US-08-046-160-2	 Sequence 2, Appli
w	828	49.1	315	σ	US-08-224-594-2	Sequence 2, Appli
. 4	828	49.1	315	14	US-08-932-194-2	Sequence 2, Appl
υı	828	49.1	315	14	US-08-932-194A-2	Sequence 2, Appl
6	706	41.8	. 329	13	US-08-838-418-2	Sequence 2, Appl

ALIGNMENTS

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INTERPORTED TO CART	RESULT 1 PCT-US98-18626-2 Sequence 2, Ap GENERAL INFOR APPLICANT:
TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF COMPUTER MEDIUM MEDIUM MEDIUM MEDIUM COMPUTER OPERAT OPERAT OPERAT CURRENT LAPPLIC FILING CLASSI PRIOR AP PRIOR AP PRIOR AP TELECOMM	1 98-1 ence ERAI PPLI
TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: COMPUTER READABLE FO MEDIUM TYPE: IBM 9C OPERATING SYSTEM: SOFTWARE: ASCII T CURRENT APPLICATION NUMBER APPLICATION NUMBER FILING DATE: 08 S CLASSIFICATION NUMBER FILING DATE: 17 S AFPLICATION NUMBER FILING DATE: 17 S AFFORNEY/AGENT INFOOR NAME: REMILLARD, REGISTRATION NUMBER FILEGAX: (617) TELECOMMUNICATION IN TELEPHONE: (617) TELETAX: (617) TELETAX: (617) TELETAX: (617)	ULT 1 -US98-18626-2 equence 2, Applicati general INFORMATION: APPLICANT:
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TITLE OF INVENTION: METHODS AND COMPITELE OF INVENTION: AND TREATING MALL NUMBER OF SEQUENCES: 20 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US98/18626 FILLING DATE: 08 SEPTEMBER 1998 CLASSIFICATION DATA: APPLICATION NUMBER: US 08/932,194 FILING DATE: 17 SEPTEMBER 1997 ATTORNEY/AGENT INFORMATION: NAME: REMILLARD, JANE E. REGISTRATION NUMBER: B. REGISTRATION NUMBER: DCI-103PC TELECOMMUNICATION INFORMATION:	SULT 1 T-US98-18626-2 T-US98-18626-2 Sequence 2, Application PC/TUS9818626 GENERAL INFORMATION: APPLICANT:
METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING MALARIA 20 M: yy disk yy disk compatible PC-DOS/MS-DOS xxt xxt xxt PCT/US98/18626 PCT/US98/18626 PCTFEMBER 1998 PTEMBER 1997 AATA: US 08/932,194 PTEMBER 1997 AATION: AND E. 1: 38.872 103.PC OGMATION: 227-7400 24214 NO: 2: TCS:	SSNL,
Dle Dle DMS-DO DMS-DO R 1998 8/932, R 1997 R 1997 R 1997 R 1997	9818
AND COMPATING MAL ATING MAL Le MS-DOS MS-DOS 1998 1998 1997 1997 1997 1997	526
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Result
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440.5
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423.5
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o55383 synechocyst
o67655 aquifex aeo
067581 aquifex aeo
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044340 styela plic
049191 arabidopsis
o23569 arabidopsis
o23569 arabidopsis
o93547 harpagifer
093545 lepidonotot
059244 bacillus ca
093541 champsoceph
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093541 patagonotot
099768 notothenia
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093540 gobionototh
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69 SNSYE-CLKGADVVIITAGITKIPGKSDKEWSRMDLLÞVNIKIMREVGAAIKSYCPNAFV 127 	9 RPKIAMVGSGMIGGTMAFLCSLRELGDVVLFDVVPNNPMGKANDISHNSSVVDTGITVYG 68 : : : :	Query Match Best Local Similarity 60.4%; Pred. No. 3.3e-72; Matches 194; Conservative 55; Mismatches 71; Indels 1; Gaps 1;	Oxidoreductase. SEQUENCE 329 AA; 35548 MW; F06387B5AC0E6BBB CRC64;	PRINTS; PRO0086; LLDHDRGNASE.	INTERPRO; IPRO01557; -		": CATALYTIC ACTIVITY: (S)-LACTATE + NAD(+) = PYRUVATE + NADH. EMBL; U35118; AAC47443.1;		Toxopiasma gondli expresses two distinct lactate dehydrogenase homologous genes during its life cycle in intermediate hosts ".		MEDLINE; 97169139.	SEQUENCE FROM N.A. STRAIN=ME49;	[1]	Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae; Toxoplasma.	gondii:		YDROGENASE (01-MAY-2000 (TrEMBLIEL 03, Last sequence update)	(TrEMBLrel. 03,	*	P90613 PRELIMINARY; PRT: 329 AA	ICT 1
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Matches 159
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Eukaryota; Viridiplantae; Chlorophyta;
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01-JUN-2000 (TremBLrel.
MALATE DEHYDROGENASE.
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INTERPRO; IPR001236; -.
INTERPRO; IPR001557; -.
PFAM; PF00056; ldh; 1.
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Submitted (DEC-1996) to the
EMBL; U80676; AAB38970.1; -.
HSSP; Q27743; 1CET.
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01-NOV-1996 (
01-JUN-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nal
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugiura M., Tabata S.;

"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
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SEQUENCE 324 AA; 34345 MW;
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Bacteria; Cyanobacteria; Chroococca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
2-KETOACID DEHYDROGENASE (MALATE DEHYDROGENASE, LACTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-PCC6803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO;
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                                 251
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                                                                                                                                                                                                                                                                                                                                                                                                     11 KIAMVGSGMIGGTMAFLCSLRELGDVVLFDVVPNMPMGKAMDISHNSSVVDTGITVYGSN 70
IQMAESYLKDRKRVMVCSCYLQGQYGVQNHYLGVPCVIGGRGVEKIIELELTAQERQELQ
                                                                     MLPLPRYCTVSGVPITEL-----IPPOTIEELVERTRNGGAEIAALLQTGTAYYAPASSA
                                                                                                   MVPLSRYATVNGIPLSEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYYAPGASA 250
                                                                                                                                                                                                TNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVIGVHGDH 190
                                                                                                                                                                                                                                                                     EYEATAGSDVVVITAGLPRRPG-----MSRDDLLGKNANIVAQGAREALRYSPNAILIVV
                                                                                                                                                                                                                                                                                                 SYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAFVINI 130
                                                                                                                                                                                                                                                                                                                                                                    QVTVVGAGNVGRTLAQRLVQQNVANVVLLDIVPGLPQGIALDLMAAQSVEEYDSKIIGTN
                                                                                                                                                                    TNPLDVMTYLAWKVTGLPSQRVMGMAGVLDSARLKAFIAMKLGACPSDINTLVLGGHGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128;
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IPR001557; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 634;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
.8e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechocystis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 324;
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ing regions.";
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Query Match
Best Local s
Matches 132
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Graham D.E., Overbeek R.
Feldman R.A., Short J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MALATE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998
01-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aquifex aeolicus
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                                                                                                                       T-SAYYAPAAAIVDMIEALVQNSKRILPCSVYLDGEAGEYYGVQGFCVGVPVKLGSNGVE
                                                                                                                                    QGSAYYAPGASAIQMAESYLKDRKRVMVCSCYLQGQ----YGVQNHYLGVPCVIGGRGVE
                                                                                                                                                                                                                                      KSYCPNAFVINITNPLDYMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRD
                                                                                                                                                                                                                                                                                       TVYG-----SNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAI
                                                                                                                                                                                                                                                                                                                        VAVIGAGNVGEHVASLILLKNLANVKMFDLPRKTEEKVFEPVKGKALDMKQMLAAMDIDA
                                                                                                                                                                                                                                                                                                                                               IAMVGSGMIGGTMAFLCSLRELGDVVLFDV------VPNMPMGKAMDISHNSSVVDTGI
                                                                          EIIKVPMIEEEREMWRRSVESVKKTVEVAEGILSAGSSR
                                                                                                  KIIELELTAQERQELQGSIDEVK---
                                                                                                                                                                         IHAYVIGGUGDEMVPLISISNVGGIPLKDLLPK----EKLEKIIERTRFGGGEIVNLMG
                                                                                                                                                                                                                        KRYAPDAIVIVVTNPVDVMTYVAYKLLNFPKNRVMGMAGVLDSARFKTFISEELMVSPKD
                                                                                                                                                                                                                                                                         RVEGYTVTPEGEGYEPLEGSDIVVITAGFPRRPG-----MSREDLLEANIRIISVIADRI
                                                                                                                                                                                            VQGMVIGVHGDHMVPLSRYATVNGIPLSEFVKKGWIKQEEVDDTVQKTKVAGGEIVRLLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE000756; AA0
Q27743; 1CET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVMVESILRNQSRILPAATYLDGAYGLKDIFLGVPCRLGCRGVEDILEVQLTPEEKAALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392:353-358(1998).
AE000756; AAC07619.1;
                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      00056; ldh; 1:
PS00065; D_2_HYDROXYACID_DH_1; UNKNOWN_1.
PS00867; CPSASE_2; UNKNOWN_1.
PS00867; CPSASE_3; E02FA4C339237118 CR
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                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                              Conservative.
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                                                                                                                                                                                                                                                                                                                                                                                          35.9%;
38.9%;
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J.M., Olson G.J., Swanson R.V.;
of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aquificaceae;
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Olson
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                PRT;
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annotation update)
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              AA.
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Best Local
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                                                                                                                                                         01-JUN-1998
01-JUN-1998
01-JUN-2000
                                                                                                                                                                                             044340;
                                                                                          Styela plicata (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea
Stolldobranchia; Styelidae; Styela.
   Stock D.W., Quattro J.M., Whitt G.S., Powers D.A., "Lactate dehydrogenase (LDH) gene duplication during evolution: the cDNA sequence of the LDH of the tunical
                                                                                                                                          01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-2000 (TrEMBLrel. 14, L-LACTATE DEHYDROGENASE (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998
01-AUG-1998
01-MAY-2000
                                 MEDLINE; 980
Stock D.W.,
                                                         TISSUE-BODY
                                                                                                                    Styela plicata (Sea
                                                                                                                                    LDH
L
                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deckert G., Warren P.V., Gaastella
Graham D.E., Overbeek R., Snead M.
Graham D.E., Short J.M., Olson G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00056; SEQUENCE 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000750; AAI
HSSP; Q27743; 1CET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 392:353-358(1998).
EMBL; AE000750; AAC07547.
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Bacteria; Aquificales;
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01-AUG-1998 (TIEMBLIGE).
01-MAY-2000 (TIEMBLIGE).
MALATE DEHYDROGENASE.
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hes 121;
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                                                                                                                                                                                                                                                                                            IIELELTAQERQELQGSIDEVKEM
                                                                                                                                                                                                                                                                                                                               GSAYYAPGASAIQMAESYLKDRKRVMVCSCYLQGQ----YGVQNHYLGVPCVIGGRGVEK
                                                                                                                                                                                                                                                                                                                                                                 QGMVIGVHGDHMVPLSRYATVNGIPLSEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPKIAMVGSGMIGGTMAFLCSLRELGDVVLF-----DVVPNMPMGKAMDISHNSSVVDTG 63
                                                                                                                                                                                                                                                                                                                                                                                                                 INVKGISYDKEGFEELKGSDIVVITAGIPRREG-----MSREDLLYENLKILKKFTDAIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITV----YGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIK 119
                                                                                                                                                                                                                                                                                                                 -SAYYAPAASVVIMVESIINDRKRVMPCSVYVEGEAAKHYEIEGVCIGLPVVLGKKGVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity.
                                           98066358
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                                                                                                                                                                                                          PRELIMINARY;
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AA;
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                                                                                                                                       Last sequence update)
Last annotation update)
1.1.1.27) (LACTIC ACID
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                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 569;
Pred. No. 5.
                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                     323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18E64807D16B7C96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Keller M., Auj
Swanson R.V.;
                                                                                                                                                                                                       338
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.9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101;
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                                                                                                                                         DEHYDROGENASE).
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  Styela
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                                                                                                                                                                                                                                                                                                                                    049191 PRELIMINARY; PRT; 353 AA.
049191;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
11-JUN-2000 (TrEMBLrel. 14, Last annotation update)
11-ACTATE DEHYDROGENASE (EC 1.1.1.27) (L-LACTATE DEHYDROGENASE)
                                                                                                             DOIFerus R. Peacock W.J., Dennis E.S.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: (S) LACTATE + NAD(+) = PYRUVATE
EMBL; AF043130; AAC02678.1; -.
HSSP: P00339; 9LDB.
MENDEL; 28075; Arath; 1258; 28075.
                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids II;
Oxidoreductase. seouence 353 AA;
                                                                                                                                                                                                          STRAIN=CV. ECOTYPE C24;
                                                                                                                                                                                                                                                     Brassicaceae; Arabidopsis.
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INTERPRO: IPR001557; -.
PFAM: PF00056; ldh; l.
PR1NTS; PR00086; LLDHDRGNASE.
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-:- CATALYTIC ACTIVITY: (S)-LACTATE + NAD(+) = PYRUVATE + NADH.
EMBL, AF023168; AAC02943.1; --
HSSP; P00339; 9LDB.
                              PROSITE; PS00064; L_LDH;
                                                                                                                                                                                                                                                                                                                              (LACTIC ACID
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                                               PRINTS; PR00086; LLDHDRGNASE
                                                         PFAM; PF00056;
                                                                         INTERPRO; IPR001236; -.
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                                                                                                  NTERPRO; IPRO00205; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVHGDHMVPLSRYATVNGIPLSEFVKK-----GWIKQEEVDDIVQKTKVAGG-EIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLGQGSAYYAPGASAIQMAESYLKDRKRVMVCSCYLQGQYGVQNHY-LGVPCVIGGRGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEHGDSSVPMWSGVNVSGKCLNSIHPRIGYPDGPEGW-----DKIHKQVVDGAYDVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AILVIVSNPVDLMTYVAWKLSNFPRNRVIGSGTNLDSARFRHLIAEKLNLSPVSVHGWII 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVYGDKDYSVSANSRIVIVTAGARQQPGE----SRLSLVQRNVNIFKHIIPQIAKYSPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIIELELTAQERQELQGSIDEVKEMQKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L--KGYTNWAIGLSCAELLATILHHRHRIHPVTCFVKGRYGITDDVCLSLPCVLNCNGVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSGPSKVTVVGVGMVGMACGMSVVLKGLCTDLVLVDVVQDKLQGEVMDLQHGSLFLE-NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 AA;
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                                                                                                                                                                                                                                                                                                                            DEHYDROGENASE).
                                                           1dh; 1
    37936 MW;
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Pred. No. 6.7e-27;
9; Mismatches 128
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   359FCDD3CF31260E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323
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Brassicales;
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Best Local Similarity
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023569;
01-JAN-1998;
01-JAN-1998;
01-JUN-2000
                                                                                                                                                                                                                                                                                         Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,
Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,
Ridley P., Hudson S.A., Patel K., Wurphy G., Piffanelli P., Wedler H.,
Wedler E., Wambutt R., Weitzenegger T., Pohl T.M., Terryn N.,
Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,
Entian K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,
                                                                                                                        Schueller C., Chalwatzis N.;
Analysis of 1.9 Mb of contiguous
Arabidopsis thaliana.";
Nature 391:485-488(1998).
EMBL; 297343; CABI0507.1; -.
HSSP; P00339; 9LDB.
                                                                                                                                                                                                                             Silvey M., James R., Montfort A., Pons A., Puigdomenech P., Douka A. Voukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermaier Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T., Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 98121113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Embryophyta;
                PFAM; PF00056; ldh; 1.
PRINTS; PR00086; LLDHDRGNASE.
PROSITE; PS00064; L_LDH; 1.
                                                                                                           MENDEL; 26784; Arath;1258;26784.
                                                                                                                                                                                                                 Delseny M., Voet M., Volckaert G., Mewes H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Embry Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LACTATE DEHYDROGENASE
                                                            INTERPRO; IPRO01557;
                                                                                           NTERPRO;
                                                                            NTERPRO; IPRO01236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVHGDHMVPLSRYATVNGIPLSEFVKKGWIKQEE--VDDIVQKTKVAGGEIVRLLGQGSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T--ASVDYEVTAGSDLCIVTAGARQNPGE-----SRLNLLQRNVALFRHIIPPLAKASPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106;
              PS00064; L_LDH;
                                                                                           IPR000205;
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8 (TrEMBLrel. 05,
0 (TrEMBLrel. 14,
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_LDH; 1.
37950 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.1%; Score 440.5; DB 1 32.8%; Pred. No. 4.6e-26;
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Last annotation update
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosidae;
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                                                                                                                                                                                    sequence
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; eurosids II;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                 Klosterman
                                                                                                                                                                                    chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta;
Brassicales;
                                                                                                                                                                                  4 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                               Douka A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Best Local S
Matches 106
                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                      Fields P.A., Somero G.N.;
"Hot spots in cold adaptation: lactate dehydrogenase-A (A4-LDH) orthologs of antarctic notothenioid fishes.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF079820; AAC63278.1; -.
HSSP; P00339; 9LDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harpagifer antarcticus.

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthoptery
Percomorpha; Perciformes; Notothenioidei; Harpagiferidae; Harpagi
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01-JUN-2000
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                                                                                                                                                                                                                                                               Oxidoreductase.
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                                                                                                                                                                                                                                                                                PROSITE: PS00064; L_LDH;
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                                                                                                     TRPKIAMVGSGMIGGTMAFLCSLRELGD-VVLFDVVPNMPMGKAMDISHNSSVVDTGITV 66
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              -GDKDYSVTANSKVVVVTAGARQQEGE--
                                            YGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAF 126
                                                                               SRNKVTVVGVGMVGMASAISILIKDLGDELAMVDVMEDKLKGEVMDLQHGSLFLKTKIV-
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31.1%;
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08,
14,
(EC
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Last annotation update)
1.1.1.27).
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                                                                                                                                                                         Score 430.5;
Pred. No. 2.
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Pred. No. 4.6e-26
5; Mismatches 12
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                                                                                                                                                        Mismatches
                                                                                                                                                                     No.
           -SRLNEVQRNVNIFKFIIPNIVKYSPNCI 131
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                                                                                                                                                                       .4e-25;
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idae; Harpagifer.
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Best Local Similarity 31.7
Matches 103; Conservative
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093545;
01-NOV-1998
01-NOV-1998
01-JUN-2000
LACTATE DEHY
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SEQUENCE 331
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                                          240
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                                 GSAYYAPGASAIQMAESYLKDRKRYMYCSCYLQGQYGVQNH-YLGVPCVIGGRGVEKIIE
                                                                                                                                                                   VINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVIGV 186
       TS-
                                                                                                       HGDHMVPLSRYATVNGIPLSEFVKKGWIKQEEVDD-----IVQKTKVAGG-EIVRLLGQ
                                                                                                                                          LMVVSNPVDILTYVAWKLSGFPRHRVIGSGTNLDSARFRHLIGEKLHLHPSSCHAWIVGE
                                                                           HGDSSVPVWSGVNVAGVSL----
-WAIGMSVADLVESIIKNMHKVHPVSTLVQGMHGVKDEVFLSVPCVLGNSGLTDVIH
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31.7%;
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                                                                       -QGLNPQMGTEDDGENWKAIHKEVVDGAYEVIKLKGY
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Eukaryota; Metazoa; Chordata; Craniata; Ve
Actinopterygii; Neopterygii; Teleostei; Eu
Percomorpha; Perciformes; Notothenioidei;
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-GDKDYSVTANSKVVVVTAGARQQEGE-----SRLNLVQRNVNIFKFIIPNIVKYSPNCI 131
                                  YGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAF 126
                                                                 SRSKVTVVGVGMVGMASAISILLKDLCDELAMVDVMEDKLKGEVMDLQHGSLFLKTKIV-
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Euteleostei; Acanthoptery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nototheniidae;
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Best Local
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PROSITE; PS00064; L_LDH; 1.
Oxidoreductase; NAD; Glycolysis.
ACT_SITE 179 179
BY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zuelli F., Weber H., Zuber H.,

"Structure and function of L-lactate dehydrogenases from thermophilic and mesophilic bacteria, VI. Nucleotide sequences of lactate dehydrogenase genes from the thermophilic bacteria Bacillus dehydrogenase genes from the thermophilic bacteria Bacillus stearrothermophilus, B. caldolyticus and B. caldotenax.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 88050101.
Zuelli F., Weber H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus caldolyticus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel 01, 01-NOV-1996 (TrEMBLrel 01, 01-JUN-2000 (TrEMBLrel 14, L-LACTATE DEHYDROGENASE (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00056; ldh; 1.
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CATALYTIC ACTIVITY: L-LACTATE + NAD(+) = PYRUVATE + NADH
PATHMAY: FINAL STEP IN ANAEROBIC GLYCOLYSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HOMOTETRAMER
                                                                                         AQERQELQGSIDEVKEM
                                                                                                                                       YYAPGASAIQMAESYLKDRKRYMYCSCYLQGQYGVQNHYLGVPCVIGGRGVEKIIELELT 302
                                                                                                                                                                                                                            QGLFLVATNPVDILTYATWKFSGLPHERVIGSGTILDTARFRFLLGEYFSVAPQNVHAYI
                                                                                                                                                                                                                                                                                  ADIWHGDYDDC-RDADLVVICAGANQKPGE----TRLDLVDKNIAIFRSIVESVMASGF
                                                                                                                                                                                                                                                                                                                                       RNNGGTRVVVIGTGFVGASYAFALMNQGIADEIVLIDANESKAIGDAMDFNHGKVFAPKP
                                                                                                               YYGIAMGLARVTRAILHNENAILTVSAYLDGPYGERDVYIGVPAVINRNGIREVIEIELN 293
                                                                                                                                                                                    IGVHGDHMDPLSRYATVNGIPLSEFVK-KGWIKQEEVDDIVQKTKVAGGEIVRLLGOGSA 242
                                                                                                                                                                                                                                            NAFVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMV 183
                                                                                                                                                                                                                                                                                                           ITVYGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCP 123
                                                                                                                                                                                                                                                                                                                                                                   EKNTRPKIAMVGSGMIGGTMAFLCSLRELGD-VVLFDVVPNMPMGKAMDISHNSSVVDTG
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                                                               DDEKNRFHHSAATLKSV
                                                                                                                                                                      IGEHGDTELPVWSQADIGGVPIRKLVESKGEEAQKELERIFVNVRDAAYQIIE--KKGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTLKAEEEKQLQKSAETLWGVQKEL 329
                                                                                                                                                                                                                                                                                                                                                                                              92; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 AA;
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29.0%; Pred
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Last annotation update)
1.1.1.27).
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                                                                                                                                                                                                                                                                                                                                                                                                Score 428; DB 2;
Pred. No. 3.6e-25;
7; Mismatches 138
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093619;
01-NOV-1998
01-NOV-1998
01-JUN-2000
Trematomus bernacchii.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygercomorpha; Perciformes; Notothenioidei; Channichthyidae;
                                                      Chionodraco rastrospinosus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "HOL spots in cold adaptation: lactate dehydrogenase-A (A4-LDH) orthologs of antarctic notothenioid fishes."; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF079824; AAC63282.1; -. HISSP; P00335; 5LDH.
                                                                      LDH-A.
                                                                               LACTATE DEHYDROGENASE-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKATYOTA: METAZOA; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Percomorpha; Perciformes: Notothanicia
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                                                                                                                                                                                                         VIHMTLKAEEEKQLQKSAETLWGVQKEL
                                                                                                                                                                                                                                                      KGYTS--WAIGMSVADLVESIIKNMHKVHPVSTLVQGMHGVKDEVFLSVPCVLGNSGLTD
                                                                                                                                                                                                                                                                               LGQGSAYYAPGASAIQMAESYLKDRKRVMVCSCYLQGQYGVQNH-YLGVPCVIGGRGVEK
                                                                                                                                                                                                                                                                                                                             HGDHMVPLSRYATVNGIPL-----SEFVKKGW--IKQEEVDDIVQKTKVAGGEIVRL 236
                                                                                                                                                                                                                                                                                                                                                          LMVVSNPVDILTYVAWKLSGFPRHRVIGSGTNLDSARFRHLIGEKLHLHPSSCHAWIVGE
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                                                                                                                                                                                                                                                                                                                                                                                                         -GDKDYSVTANSKVVVVTAGARQQEGE-----SRLNLVQRNVNIFKFIIPNIVKYSPNCI
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                                                                                                                                                                                                                                                                                                        HGDSSVPVWSGVNVAGVSLQGLNPQMGTEGDGENWKAIHKEVVD-----
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                                                                                           (TrEMBLrel.) (TrEMBLrel.)
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                                                    Chaenocephalus aceratus,
                                                                                        Last sequence update)
                                                                                                                    Created)
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Euteleostei; Acanthoptery
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Best Local Similarity
                                                                                              093546;
01-NOV-1998
01-NOV-1998
01-JUN-2000
                                     Eukaryota; Metazoa; Chordata; Actinopterygii; Neopterygii; Percomorpha; Perciformes; Not
                                                                                    01-NOV-1998 (TrembLrel.
01-NOV-1998 (TrembLrel.
01-JUN-2000 (TrembLrel.
LACTATE DEHYDROGENASE-A
                                                                                                                                    093546
   TISSUE-MUSCLE;
                                                                Patagonotothen tessellata
                                                                             LDH-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fields P.A., Somero G.N.;
"Hot spots in cold adaptation: lactate dehydrogenase-A (
"Thougs of antarctic notothenioid fishes.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
            SEQUENCE FROM N.A.
                        Patagonotothen.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oxidoreductase. SEQUENCE 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00064; L_LDH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00056; 1dh;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cold adaptation in lactate Submitted (JUL-1999) to the EMBL; AF079829; AAC63287.1; EMBL; AF079819; AAC63277.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=T.BERNACCHII;
Marshall C.J., Love C
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                                                                                                                                                                                                                                                                         HGDHMVPLSRYATVNGIPL------SEFVKKGW--IKQEEVDDIVQKTKVAGGEIVRL
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                                                                                                                                                                                                                                                                                                                                                                                      TRPKIAMVGSGMIGGTMAFLCSLRELGD-VVLFDVVPNMPMGKAMDISHNSSVVDTGITV 66
                                                                                                                                                                                                                   KGYTS--WAIGMSVADLVESTIKNMHKVHPVSTLVQGMHGVKDEVFLSVPCVLGNSGLTD
                                                                                                                                                                                                                                                        HGDSSVPVWSGVNVAGVSLQGLNPQMGTEGDGENWKAIHKEVVD
                                                                                                                                                                                                                                                                                           LMVVSNPVDILTYVAWKLSGFPRHRVIGSGTNLDSARFRHLIGEKLHLHPSSCHAWIVGE
                                                                                                                                                                                                                                                                                                                                                 YGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAF 126
                                                                                                                                                                                                                                                                                                                                                                      SRNKVTVVGVGMVGMASAISILLKDLCDELAMVDVMEDKLKGEVMDLQHGSLFLKTKIV-
                                                                                                                                                                                                                                                                                                                                  -GDKDYSVTANSKVVVVTAGARQQEGE----
                                                                                                                                                                                                                                                                                                                                                                                                            103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P00336; 5LDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF170847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR00086; LLDHDRGNASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .RASTROSPINOSUS; TISSUE=MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD48487.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         36183 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                    25.3%;
31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-WHITE MUSCLE,
                                                                                    08,
08,
14,
(EC
                                      Notothenioidei;
                                                                                                                                                                                                                                                                                                                                                                                                            68;
                                                                                  Last sequence update)
Last annotation update)
1.1.1.27).
                                                                                                                                                                                                                                                                                                                                                                                                           Score 426.5; DB 1
Pred. No. 4.9e-25;
68; Mismatches 128
                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dehydrogenases
                                               Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        6C626409CA0FDAE9 CRC64;
                                                                                                                                                                                                                                                                                                                                SRLNLVQRNVNIFKFIIPNIVKYSPNCI
                                                                                                                                  331
                                              Euteleostei;
                                                       Vertebrata; Euteleostomi;
                                                                                                                                  Ã
                                      Nototheniidae;
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from
                                                                                                                                                                                                                                                                                                                                                                                                           128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antarctic
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 331;
                                             Acanthopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (A4-LDH)
                                                                                                                                                                                                                                                       -GAYEVIKL
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RESULT
Q9PRH8
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Best Local :
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"Cold adaptation in lactate Submitted (JUL-1999) to the EMBL; AF170848; AAD48488.1; EMBL; AF170846; AAD48486.1; INTERPRO: IPRO01236; -
                                                                                   TISSUE-WHITE MUSCLE;
Marshall C.J., Fleming R.I.;
                                                                                                                                                                  Notothenia angustata (Rockcod), and pagothenia borchgrevinki (Bald rockcod) Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei;
                                                                                                                                                                                                                                                                                                                                          Q9PRH8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Hot spots in cold adaptation: lacta orthologs of antarctic notothenioid Submitted (JUL-1998) to the EMBL/Gen EMBL; AR079830; AAC63288.1; -HSSP; P00339; 9LDB.
                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                      01-JUN-2000
LACTATE DEHI
                                                                                                                                                                                                                                                                                                                         Q9PRH8;
                                                                                                                                                      Percomorpha;
                                                                                                                                                                                                                                          LDH-A
                                                                                                                                                                                                                                                                                       01-MAY-2000
                                                                                                                                                                                                                                                                                                           01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase. SEQUENCE 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00056; ldh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fields P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                          302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITELELTAQERQELQGSIDEVKEMQKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGQGSAYYAPGASAIQMAESYLKDRKRVMVCSCYLQGQYGVQNH-YLGVPCVIGGRGVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGDHMVPLSRYATVNGIPL-----SEFVKKGW--IKQEEVDDIVQKTKVAGGEIVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMVVSNPVDILTYVAWKLSGFPRHRVIGSGTNLDSARFRHLIGEKLHLHPSSCHAWIVGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRSKVTVVGVGMVGMASAISILLKDLCDELAMVDVMEDKLKGEVMDLQHGSLFLKTKIV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRPKIAMVGSGMIGGTMAFLCSLRELGD-VVLFDVVPNMPMGKAMDISHNSSVVDTGITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGYTS--WAIGMSVADLVESIIKNMHKVHPVSTLVQGMHGVKDEVFLSVPCVLGNSGLTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGDSSVPVWSGVNVAGVSLQGLNPQMGTEGDGENWKAIHKEVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GDKDYSVTANSKVVVVTAGARQQEGE-----SRLNLVQRNVNIFKFIIPNIVKYSPNCI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al Similarity
102; Conserv
                                                                                                                                                                                                                                                 2000 (TrEMBLrel. 13, Last sequence update) 2000 (TrEMBLrel. 14, Last annotation updat DEHYDROGENASE-A (EC 1.1.1.27).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 AA;
                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                      Perciformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Somero G.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adaptation: lactate dehydrogenase-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36142 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.1%;
                                                                                                                                                   Notothenioidei;
                    69;
                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 424.5; DE Pred. No. 7e-25;
                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45BF26DC3A03237E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       323
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                                                                                                                                                                  Vertebrata; I
Euteleostei;
                                                                                                                                                                                                   (Trematomus
                                                                                                                                                                                                                                                                                                                                      3
                                                                                                                                                 Nototheniidae;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128;
                                                                  Antarctic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                borchgrevinki).
Euteleostomi;
                                                                                                                                                 Acanthopterygii;
dae; Notothenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (A4-LDH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GAYEVIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
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PRINTS; PR00086; LLDHDRGNASE PROSITE; PS00064; L_LDH; 1.

AA;

36169 MW;

7CB80409CA0FDAE9 CRC64;

INTERPRO; IPR001557 PFAM; PF00056; 1dh;

IPR001557; -.

Query Match 25.1%; Score 423.5; DB 13; Length 331; Best Local Similarity 31.1%; Pred. No. 8.4e-25; Matches 102; Conservative 69; Mismatches 128; Indels 29; Gaps 8 TRPKIAMVGSGMIGGTMAFLCSLRELGD-VVLFDVVPNMPMGKAMDISHNSSVVDTGITV 66; : : : : : :

Search completed: November 15, 2000, 09:47:45
Job time: 61 sec

us-08-676-882-2.rsp

OM protein - protein search, using sw model Wed_Nov sequence: Title: perfect score: Scoring table: Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 20000000000 post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries 15 09:51:35 us-08-676-882-2 1688 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. November 15, 2000, 09:47:23; BLOSUM62 Gapop 10.0 , Gapext 0.5 87993 seqs, 31947931 residues MAVFEKNTRPKIAMVGSGMI.........GSIDEVKEMQKAIAALDASK 330 2000 ; Search time 11.5 Seconds (without alignments) g16.767 Million cell updates/sec 87993 LDH_TOXGO 34 35 36 37 38 39 40 41 LDH_TOXGO 027797; 01-NOV-1997 405 402 402 402 401 400 400 400 399 399 23.8 23.8 23.8 LDHM_PIG LDHA_XENLA LDH_LACPE LDHX_VULVU

LDHH_MOUSE MDH_ARCEU LDHC_XENLA LDHX_RAT

p16125 mus musculu p42123 rattus norv p42123 rattus norv p19858 bos taurus p04642 rattus norv

Q92055 fundulus he

008349 archaeoglob 029563 vulpes vulp p42121 xenopus lae

rattus norv

P42120 P56511

) xenopus lae lactobacill

sus

scrofa

LDHA_FUNHE LDHM_BOVIN LDHM_RAT

ALIGNMENTS

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CCCCCCCCCCCR = 4 4 4 4 8 6 6 6 6 5 B
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
L-LACTATE DEHYDROGENASE (EC 1.1.1.27) (LDH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxoplasma gondii.
Eukaryota: Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE: 96123406.

Yang S., Parmley S.F., Controlly expressed gene of Toxoplasma Yang S., Parmley S.F., Controlly expressed gene of Toxoplasma Yang S., Parmley S.F., Controlly Expressed gene of Toxoplasma Yang S.F., Controlly Expected Parasitol 73:291-294(1995).

encodes a polypeptide homologous 1924(1995).

encodes a polypeptide 173:291-294(1995).

PATHWAY: PARASITOL 73:291-294(1995).

PATHWAY: FINAL STEP IN ANAEROBIC GLYCOLYSIS.

CATALYTIC ACTIVITY: L-LACTANER (BY SIMILARITY).

1. PATHWAY: HOMOTETRAMER (BY SIMILARITY).

1. SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roxoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration with the Swiss Institute of Bioinformatics and the Emergence of the European Bioinformatics in Institute. There are no restrictions on way the European Profit institutions as long as its content is in no way use by non-profit institutions as long as its content of commercial use by non-profit institutions along as its content of commercial use by non-profit institutions along the by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is content (See http://www.isb-sib.ch/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/entities a license agreement (See http://www.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: U23207; AAC46863.1; -.
HSSP: Q27743; ILDG:
                                                                                                                                            INTERPRO: LLDHORONASE.
PFAM: PF00056; LLDHORONASE.
PFAM: PF00086; LLDHORONASE.
PRINTS: PR00084; L_LDH; FALSE_NEG.
PRINTS: PS00064; L_LDH; FALSE_NEG.
PROSITE: PS00064; L_CDH; FALSE_NEG.
PROSITE: PS00064; L_CDH; FALSE_NEG.
PROSITE: PS00064; LCCEPTS A PROTON DURING CATALYSIS
PROSITE: NAD: Glycolysis
OXIdoreductase: NAD: Glycolysis
                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO; IPRO01557;
                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERPRO: IPRO01236; ..
                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                        326 AA;
Score 1072: DB 1;
pred. No. 1.5e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326
                                                                                     DB 1;
                                                                                             Length 326;
                                                           Gaps
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patabase :

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score distribution. and is derived by analysis of the total score distribution.

Result NO.

score

Query Match Length DB

MDH_RHILV LDH1_PLAFD LDH_TOXGO

027797 toxoplasma 033525 rhizobium 1 033525 rhizobium 027743 plasmodium 09zdf3 rickettsia 09zdf3 bacillus su p49814 bacillus su

Q59202 bacillus is Q9x4k8 bacillus th p80040 chloroflexu

Description

MDH_RICPR

MDH_BACTC MDH_BACIS MDH_BACSU

MDH_CHLAU

MDH_AERPE WDH_CHLVI MDH_CHLTE

> Q9yeal aeropyrum p p13714 bacillus su p80038 chlorobium p80039 chlorobium

p00345 bacillus me

5 thermotoga

bacillus ps

LDH_BACME _DH_BACSU

LDH_MYCGE DH_THEMA DHP_BACPS 826.5

628 607.5 560 -5

42. 40. 37

439

430. 428.

LDH_LACCA

DHX_MOUSE LDH_MYCPN DH_BACCA

UDH_BACST DHH_PIG DHC_FUNHE DHM_SQUAC

LDH_PETMA

p00338 homo sapien p42119 xenopus lae

HUMAN

LDH_LACSK LDHX_BACPS

> P00343 lactobacill p20619 bacillus ps p50934 lactobacill P47698 mycoplasma

p00342 mus musculu p10655 bacillus ca p19869 bifidobacte

Query Match Best Local S

63.5%;

Mismatches

Indels

0

Matches 199;

7 mycoplasma 4 bacillus st

fundulus he lactobacill sus scrofa

g

20

squalus aca petromyzon

420.5 423

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Page
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INTERPRO; 15...

INTERPRO; 15...

PFAM; PP00056; ldh; 1.

PRINTS; PR00066; LLDHDRGNASE.

R PROSITE; PS00068; MDH; FALSE_NEG.

TY Oxidoreductase; Tricarboxylic acid cycle; NAD.

149 149 PROTON-RELAY (BY SIMILARITY).

PROTON-RELAY (BY SIMILARITY).
                                                                                               69 SNSYECLKGADVVIITAGITKIPGKSDKEWSRNDLLPVNIKINREVGAAIKSYCPNAFVI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MDH_RHILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERPRO: IPRO01236; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ002750; CAA05717.1;
HSSP; Q27743; 1LDG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institute. There are no restrictions entities requires a license arrowed. Usage by solve is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation of the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Poole P.S., Allaway D., Smith M.;
Submitted (NOV-1997) to the EMBL/GenBank/DbBJ databases.
-! CATALYTIC ACTIVITY: HALLATE + NAD(+) OXALOACETATE + NADH.
-! SUBUNIT: HOMODIMER (BY SIMILARITY) OXALOACETATE + NADH.
-! SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
                                                                                                                                                                                  RNKIALIGSGMIGGTLAHLAGLKELGDIVLFDIADGIPQGKGLDISQSSPVEGFDVNLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=3841;
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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15-JUL-1998 (Rel. 36, Last sequence update)
30-MALATE DEHYDROGENASE (EC 1.1.1.37)
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                                                                                                                                                                                                                                                                     52.5%; Score 886.5; DB 1;
54.5%; Pred. No. 1.9e-60;
*^. Mismatches 79;
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                                                             ---MSRDDLLGINLKYMEQVGAGIKKYAPNAFVI 117
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                                                                                                                                                                                                                                           Gaps
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                                                                VARIANT
VARIANT
SEQUENCE
                                                                                                                                            PROSITE,
Oxidoreductase; N
                                                                                                                                                                                                                                             PDB; 1CEQ; 19-MAR-99.
PDB; 1CET; 19-MAR-99.
                                                                                                                                                                                                                                           PFAM; PF00056;
                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                EMBL; M93720; AAA29633.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDH1_PLAFD
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"The structure of lactate dehydrogenase from plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 93295434.
Bzik b.J. Fox B.A., Gonyer K.;
"Expression of plasmodium falciparum lactate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=HONDURAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-Nov-1997 (Rel. 35, Created)
01-Nov-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
L-LACTARE DEHYDROGENASE (EC 1.1.27) (LDH-p),
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RAY CRYSTALLOGRAPHY (1.74 ANGSTROMS).
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Q27743;
                                                                                                                                                            PRO0086; LLDHDRGNASE.
3; PS00064; L_LDH; FALSE_NEG.
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                                                                                                                                                 Glycolysis;
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                                                                                   (BY SIMILARITY)
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       D25EB863954B8FC1 CRC64;
                                                                         3D-structure.
EPTS A PROTON DURING CATALYSIS
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RESULT

γQ В

49.38;

Score 831.5;

DB

Length 316;

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Query Match Best Local S Matches

Usage

restrictions on

a collaboration Outstation

Best Loc Matches

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30-MAY-2000 (Rel. 39, C
30-MAY-2000 (Rel. 39, I
30-MAY-2000 (Rel. 39, I
MALATE DEHYDROGENASE (E
MDH OR RP376.
                                                                                                                      HSSP; Q27743; 1CET.
INTERPRO; IPRO01236; -.
INTERPRO; IPRO01252; -.
                                                                                                                                                                                        use by non-prefit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                           INTERPRO; IPR001557; -.
PFAM; PF00056; ldh; 1.
                                                                                                                                                                 EMBL; AJ235271; CAA14835.
                                                                                                                                                                                                                                                                                                   Nature 396:133-140(1998).
-!- CATALYTIC ACTIVITY: L-MALATE +
-!- SIMILARITY: BELONGS TO THE LDH
                                                                                                                                                                                                                                                                                                                                                "The genome sequence mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                    Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Eriksson A.-S., Winkler H.H., Kurland C.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 99039499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rickettsiaceae; Rickettsieae;
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                                                                                                                                                                                                                                               European Bioinformatics Institute.
                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no we
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167; Conser
                                                             PR00086; LLDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteobacteria; alpha subdivision; Rickettsiales; aceae; Rickettsieae; Rickettsia.
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                                                   Tricarboxylic
            150
153
177
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of Rickettsia pro
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, Last annotation update)
(EC 1.1:1.37).
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     acid cycle; NAD.

PROTON-RELAY (BY SIMILARITY).

SUBSTRATE CARBOXYL GROUP (BY SIMILARITY).

PROTON-RELAY (BY SIMILARITY).
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                         prowazekii and
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                                                                                                                                                                                                                    Usage
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15-JUL-1998 (Rel. 3
30-MAY-2000 (Rel. 3
                                                    This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinforma
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P49814;
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Lapidus A., Galleron
                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis
Bacteria; Firmicul
                                                                                                                               Hecker M.
                                                                                                                                         Antelmann H.,
                                                                                                                                                       MEDLINE; 97443988
                                                                                                                                                                       STRAIN-IS58
                                                                                                                                                                                   SEQUENCE OF 1-15.
                                                                                                                                                                                                             Microbiology 143:3431-3441(1997).
                                                                                                                                                                                                                           "Sequencing and functional annotation in the 200 kb rrnB-dnaB region.";
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-CCT-1996 (Rel. 34, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MALATE DEHYDROGENASE (EC 1.1.1.37) (VEGETAT
                                                                                                                                                                                                                                                                                                    A Bacteriol. 178:560-563(1996).
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SUBTILIST; BG11386; CITH.
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Best Local Similarity

      PRINTS;
      PRO0086;
      LLDHDRGNASE.

      PROSITE;
      PS00068;
      MDH;
      FALSE_NEG.

      Oxidoreductase;
      Tricarboxylic acid

      ACT_SITE
      153
      PROTO

      BINDING
      156
      SUBSTI

      ACT_SITE
      180
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      BINDING
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      SEQUENCE
      312
      AA;
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      MW;
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Q9X4K8;
30-MAY-2000
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Bacillus thermodenitrificans.

Bacteria; Firmicutes; Bacillus/
Bacteria; Firmicutes; group;
                                          Williams R.A.D.,
                                                                                 STRAIN=00462;
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 MALATE DEHYDROGENASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00056;
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IPR001557;
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                                                                                                                                                                                                                                                                                                                                             (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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PROTON-RELAY (BY SIMILARITY).
SUBSTRATE CARROXYL GROUP (BY SIMILARITY).
PROTON-RELAY (BY SIMILARITY).
; 64CE3BFF1B3C02D2 CRC64;
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Pred. No. 1.7e-48;
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MALATE DEHYDROGENASE (F
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       MEDLINE;
Synstad B
                                                                             Chloroflexus aurantiacus.
Bacteria; Green non-sulfur bacteria;
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ACT_SITE
SEQUENCE
                              STRAIN-J-
                                           SEQUENCE FROM N.A.
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PROSITE; PS00068; MDH; FALSE_NEG.
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ACT_SITE 153 153 PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dehydrogenase from 'Bacillus thermodenitrificans'.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: L-MALATE + NAD(+) - OXALOACETATE +
-!- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBBAMILY.
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IPR001252;
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312 /
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PROTON-RELAY (BY SIMILARITY).

SUBSTRATE CARBOXYL GROUP (BY SIMILARITY).

PROTON-RELAY (BY SIMILARITY).

68C691C462EFF452 CRC64;
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No. 2e-47;
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**Malate dehydrogenase from the thermophilic green bacterium Chloroflexus aurantiacus: purification, molecular weight, amino composition, and partial amino acid sequence.";

J. Bacteriol. 170:2947-2953(1988).

-I. CATALYTIC ACTIVITY: L.MALATE + NAD(+) = OXALOACETATE + NADH.
-I. SUBUNIT: HOWOTETRAMER (ACTIVE ENZYME); HOWODIMER AND HOMOTRI AT TEMPERATURES LOWER THAN 55 DEGREES CELSUS (INACTIVE FORM.).

-I. SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; Tricarboxylic acid cycle; NAD.
ACT_SITE 148 148 PROTON-RELAY (BY SIMILARITY).
BINDING 151 151 SUBSTRATE CARBOXYL GROUP (BY ACT_SITE 175 PROTON-RELAY (BY SIMILARITY).
SEQUENCE 309 AA; 32717 MW; 97743CC707F3F335 CRC64;
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INTERPRO; IPR001252; -.
INTERPRO; IPR001557; -.
PFAM; PF00056; ldh; 1.
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PROSITE; PS00068; MDH; FALSE_NEG
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292 LNASAKAVR--
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                                                                          ATAQMVEAVLKDKKRVMPVAAYLTGQYGLNDIYFGVPVILGAGGVEKILELPLNEEEMAL
                                                                                                     DHMVPLSRYATVNGIPLSEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYYAPGA
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                                        LOGSIDEVKEMOKATAALDASK
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01-NOV-1991
30-MAY-2000
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"Malate dehydrogenase from the mesophile Chlorobium vibrioforme and from the mild thermophile Chlorobium tepidum: molecular cloning, construction of a hybrid, and expression in Escherichia coli.";
J. Bacteriol. 178:7047-7052(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
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HSSP; P00344; 1LDB.
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J. Bacteriol. 174:1307-1313(1992).
i- CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Charnock C.B., Refseth U.H., Sirevag R.; "Malate dehydrogenase from Chlorobium vibrioforme, Chlorobium tepidum, and Heliobacterium gestil: purification, characterization, tepidum, and Heliobacterium gestil: purification, characterization, and investigation of dinucleotide binding by dehydrogenases by use
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               ASAIQMAESYLKDRKRVMVCSCYLQGQYGVQNHYLGVPCVIGGRGVEKIIELELTAQERQ
                                                                        GDAMVPVVKYTTVAGIPVADL--
                                                                                                              GDHMVPLSRYATVNGIPLSEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYYAPG
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Last sequence update)
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Pred. No. 8.1e-41;
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PROTON-RELAY (BY SIMILARITY).

SUBSTRATE CARBOXYL GROUP (BY SIMILARITY).

PROTON-RELAY (BY SIMILARITY).
                                                                   -ISAERIAELVERTRTGGAEIVNHLKQGSAFYSPA
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SEQUENCE
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"Malate dehydrogenase from the mesophile Chlorobium vibrioforme from the mild thermophile Chlorobium tepidum: molecular cloning, construction of a hybrid, and expression in Escherichia coli.";
J. Bacteriol. 178:7047-7052(1996).
                                                                                                                                                               ACT_
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                                                                                                                                                                                                                                                              EMBL;
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15-JUL-1998 (Rel. 36, Last sequence up
30-MAY-2000 (Rel. 39, Last anotation
MALATE DEHYDROGENASE (EC 1.1.1.37).
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01-NOV-1991 (Rel.
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                                                                                                                                     SITE
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KITVIGAGNVGATTAFRIADKKLARELVLLDVVEGIPQGKGLDMYETGPVGLFDTKIT--
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                                                 134;
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                                                                                                          PS00068; MDH; FALSE_NEG.

uctase; Tricarboxylic acid cycle; NAD.

147 147 PROTON-RELAY (BY SIMILARITY).

150 150 SUBSTRATE CARBOXYL GROUP (BY 174 174 PROTON-RELAY (BY SIMILARITY).

26 26 R -> E (IN REF. 2).

39 39 Q -> E (IN REF. 2).
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IPR001557;
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Pred. No. 2.
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Best Local Similarity
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INTERPRO; IPR601236; -.
INTERPRO; IPR061252; -.
                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                       crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
-i- CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE + NADH.
-i- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                  Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikaw. Jin no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., I Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H. Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                       Oxidoreductase;
                                                                                                   PROSITE;
                                                                                                                       PFAM; PF00056; ·ldh;
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30-MAY-2000
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PROTON-RELAY (BY SIMILARITY).
SUBSTRATE CARBOXYL GROUP (BY SIMILARITY).
PROTON-RELAY (BY SIMILARITY).
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RESULT 12
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P13714;
                EMBL; D50453;
EMBL; Z99105;
                                                                                                                     the European Bioinformatics Institute. The Large by non-profit institutions as long
                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                    or send an
                                                                                        entities
                                                                                                   modified and this statement is not removed.
                                                                                                                                                                                                                        Hediger M.A., Frank G., Zuber H.;

"Structure and function of L-lactate dehydrogenases from and mesophilic bacteria, IV. The primary structure of the lactate dehydrogenase from Bacillus subtilis.";

Biol. Chem. Hoppe-Seyler 367:891-903(1986).

-i- CATALYTIC ACTIVITY: L-LACTATE + NAD(+) = PYRUYATE +

-i- PATHMAY: FINAL STEP IN ANAEROBIC GLYCOLYSIS.
                                                                                                                                                                                                                                                                                                                                       MEDLINE; 87076052.
Hediger M.A., Fran
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
L-LACTATE DEHYDROGENASE (EC 1.1.1.27).
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Best Local S
Matches 106
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PROSITE; PS00064; L_LDH; 1.
Oxidoreductase; NAD; Glycolysis
ACT_SITE 178 BY
CONFLICT 38 38 V
CONFLICT 51 51 P
CONFLICT 57 58 GL
CONFLICT 120 120 V
CONFLICT 224 224
CONFLICT 315 318 MI
                                                                    Waldvogel S., Weber H., Zuber H.;

*Structure and function of L-lactate dehydrogenases from thermophilic and mesophilic bacteria. VII. Nucleotide sequence of the lactate dehydrogenase gene from the mesophilic bacterium Bacillus megaterium. Preparation and properties of a hybrid lactate dehydrogenase comprising moieties of the B. megaterium and B. stearothermophilus
                                                                                                                                                                                                                                                                                                                  LDH_BACME
P00345;
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Matches 101;
                                       01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation updat
L-LACTATE DEHYDROGENASE P (EC 1.1.1.27).
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Bacteria; Firmicutes; Bacillus/(
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                                  LCTA OR LDHP
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ACT_SITE 181 181 BY
SEQUENCE 318 AA; 35035 MW; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thesis (1982), ETH Zurich, Switzerland.
-!- CATALTIC ACTIVITY: L-LACTATE + NAD(+) = PYRUVATE
-!- PATHWAY: FINAL STEP IN ANAEROBIC GLYCOLYSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure and function of L-lactate dehydrogenases from thermophilic and mesophilic bacteria, V. The complete amino-acid sequence of the mesophilic L-lactate dehydrogenase from Bacillus megaterium."; Biol. Chem. Hoppe-Seyler 368:1157-1166(1987).
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                                                                                                                                                                                                                                                                                                                 AYIMGEHGDTEFPVWSHAQIGGVKLEHFINTAAIEKEPDMQHLFEQTRDAAYHIIN--RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P00344; 1LDB
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'00056; ldh; 1.
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31.7%;
Bacillus/Clostridium group;
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Pred. No. 1.
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17122190576E1485 CRC64;
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.2e-27;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0086; LLDHDRGNASE.
PROSITE; PS00064; L_LDH; 1.
Oxidoreductase; NAD; Glycolysis; Multigene family.
ACT_SITE 179 179
BY SIMILARITY.
SEQUENCE 318 AA; 35249 MW; F69165A3408E442A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as modified and this statement is not removed. Usentitles requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPRO01236; -.
INTERPRO; IPRO01557; -.
PFAM; PF00056; ldh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X55118; CAA38914.1;
PIR; S08182; S08182.
HSSP; P00344; 1LDB.
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between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schlatter D., Kriech O., Suter F., Zuber H., The primary structure of the psychrophilic from Bacillus psychrosaccharolyticus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 88134573
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MEDLINE; 90241471.
Vckovski V., Schlatter D.,
Vckovski V., Schlatter D.,
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 297
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                                                                      PGASAIQMAESYLKDRKRVMVCSCYLQGQYGVQNHYLGVPCVIGGRGVEKIIELELTAQE
                                                                                                                                                                   IAMGLARITKAILNNENSVLTVSTYLDGEYGTEDVYMGVPAVVNRNGIREIVELTLNEQE
                                                                                                 HGDTELPVW6HADIGGISITELIKRNPEYTMKDLDELFINVRDAAYQIIE--KKGATFYG
                                                                                                                         HGDHMVPLSRYATVNGIPLSEFVKKG-WIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYYA 245
                                                                                                                                                    FLIATNPVDILTYATWKFSGLPKERIIGSGTILDTGRFRFLLGEYFDIAPANVHAYIIGE
                                                                                                                                                                                                       YG--TYSDCKDADIVCICAGANQKPGE-----TRLDLVEKNLRIFKGIVEETMASGFDGI 118
                                                                                                                                                                                                                                 YGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAF 126
                                                                                                                                                                                                                                                             RVALIGAGSVGSSYAFALLNQSITE -- ELVIIDLNENKAMGDAMDLNHGKVFAPNPTKTW
ROOFKHSANVLKEI 310
                          RQELQGSIDEVKEM
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No. 1
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RESULT

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PRINTS: PRO0086; LLDHDRGNASE.
PROSITE: PS00064; LLDH; 1.
Oxidoreductase; NAD; Glycolysis; 3D-structure.
ACT_SITE 172 BY SIMILARITY.
CONFLICT 14 14 MISSING (IN REF.
                                                                                                                                           PIR;
                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                               "Lactate dehydrogenase from the hyperthermophilic be Thermotoga maritima: the crystal structure at 2.1-A reveals strategies for intrinsic protein stabilizati Structure 6:769-781(1998).
                                                                                                                                                       EMBL; X74302; CP
EMBL; AE001823;
                                                                                                                                                                                                entities requires a or send an email to
                                                                          PFAM; PF00056;
                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed.
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L-LACTATE DEHYDROGENASE (EC 1.1.1.27).
LDH OR TM1867.
                                                                                                                 TIGR; TM1867.;
                                                                                                                                                                                                                                                                                                                                                                                                                    Auerbach
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                                                                                       ENTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                        Jaenicke R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           K-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Biochem. 188:195-201(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-MSB8
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MEDLINE; 99287316.
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Lactate dehydrogenase from
                                                                                                                             S36863;
1A5Z; 23
                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                   PATHWAY: FINAL STEP IN ANAEROBIC
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                                                                                    IPR001557; -.
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                                                                                                                                                                                               email to license@isb-sib.ch).
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                                                                                                                                            S36863
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extreme thermophile Thermotoga
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QS

SEQUENCE

319 AA; 34994 MW; A1FB9B97CDCF290B CRC64;

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Query Match

Best Local Similarity. 33.2%; Pred. No. 1.8e-26;

Matches 106; Conservative 64; Mismatches 134; Indels 15; Gaps

Oy 11 KIAMVGSGMIGGTMAFLCSLRELG-DVVLFDVVPNMPMGKAMDISHNSSVVDTGITVYGS 69

II :|| || :| || :| :| || :| || || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :|
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Search completed: November 15, 2000, 09:49:26 Job time: 123 sec

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Result
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Maximum Match 100%
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ALIGNMENTS

RESULT

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Qy 305 ERQELQGSIDEVKEM 319 - - - - - - - - - - - - -	Qy 245 APGASAIOMAESYLKDRKRVMVCSCYLQGQYGVQNHYLGVPCVIGGRGVEKIIELELTAQ 304 	Qy 185 GVHGDHMVPLSRYATVNGIPLSEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYY 244	Qy 125 AFVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVI 184	Qy 65 TVYGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPN 124 : : ::	Qy 5 EKNTRPKIAMVGSGMIGGTMAFLCSLRELGDVVLFDVVPNMPMGKAMDISHNSSVVDTGI 64	Ouery Match 49.0%; Score 826.5; DB 2; Length 314; Best Local Similarity 49.8%; Pred. No. 5e-56; Matches 157; Conservative 70; Mismatches 81; Indels 7; Gaps 2;	l; GB:AJ235269; NID:g3860788; PIDN:CAA148:wadrid E	A71695 A71695 A71695 A71695 A71695 A71695 C;Species: Rickettsla prowazekii C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 20-Jun-2000 C;Accession: A71695 R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark Nature 396, 133-140, 1998 A;Title: The genome sequence of Rickettsla prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499 A;Status: preliminary; nucleic acid sequence not shown translation not shown

RESULT I40383

NAD

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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. KOetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel, Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot Reuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, Y.; Winters, P.; Wipat, A.; Yamamoto, H.; Zamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Althors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Reference number: A69580; MUID:98044033
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C:Species: Bacillus subtilis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
     malate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U05257; NID:g1045295; PIDN:AAA96343.1; PID:g1045296 R;KUNSt, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Exrington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:Z99118; GB:AL009126; NID:g2635200;
A;Experimental source: strain 168
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A.; Ehrlich, S.D.; Em
Nature 390, 249-256,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Superfamily: L-lactate dehydrogenase
;Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                           cal Similarity
147; Conserv
                                                                                                                                                                     ERQELQGSIDEVKEMQKAIA 324
                                                                                                                                                                                                                                                                                                             GGHGDDMVPLVRYSYAGGIPLETLIPK----ERIDAIVERTRKGGGEIVNLLGNGSAYY
                                                                                                                                                                                                                                                                                                                                                        GVHGDHMVPLSRYATVNGIPLSEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYY 244
                                                                                                                                                                                                                                                                                                                                                                                                       SIIVVLTNPVDAMTYAVYKESGFPKERVIGQSGVLDTARFRTFVAEELNLSVKDVTGFVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NTRKKVSVIGAGFTGATTAFLIAQKELADVVLVDIPQLENPTKGKALDMLEASPVQGFDA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTRPKIAMVGSGMIGGTMAFLCSLRELGDVVLFDV--VPNMPMGKAMDISHNSSVVDTGI 64
                                                                                                                        ERAQLNKSVESVKNVMKVLS
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Pred. No. 2.1e-49;

    Bacillus israeli

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M.; Chc
ri, E.
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A;Description: (C;Superfamily: 1C;Keywords: oxic
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C.Accession: S61213
R.Wynne, S.A.; Nicholls, D.J.; Scawen, M.D.; Sundaram, R.Wynne, S.A.; Nicholls, D.J.; Scawen, M.D.; Sundaram, R.Wynne, S.A.; Nicholls, D.J.; Scawen, M.D.; Sundaram, R.Wynne, S.A.; Nicholls, Sequence and over-expression of
                                      A; Gene: citH
                                                                   A; Cross-reférences: EMBL: D64003; A; Note: the nucleotide sequence
                                                                                                                                                           A; Reference number: S74322;
A; Accession: S75735
                                                                                                                                                                                                                                                                              C; Accession: S75735
                                                                                                                                                                                                                                                                                           C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change
                                                                                                                                                                                                                                                                                                                   C; Species: Synechocystis sp. A; Variety: PCC 6803
                                                                                                                                                                                                                                                                                                                                                probable malate dehydrogenase (EC 1.1.1.37)
N;Alternate names: 2-ketoacid dehydrogenase;
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                                                                                                                                       A; Status: nucleic acid sequence not shown;
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C; Date: 18-Sep-1997
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A; Residues: 1-312 <WYN>
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A; Accession: S61213
Superfamily: L-lactate dehydrogenase; Reywords: oxidoreductase
                                                                                                                                                                                                                             Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu,
K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.;
R. Res. 3, 109-136, 1996
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nes 141; Conservative
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                                                                                                                                                                                                         Sequence analysis of the genome of
                                                                                                                                                                                                                                                            T.; Sato,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GASAIQMAESYLKDRKRVMVCSCYLQGQYGVQNHYLGVPCVIGGRGVEKIIELELTAQER
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                                                                                                        -324 <KAN>
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                                                                   GB:AB001339;
was submitted
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                Synechocystis sp.
protein sll0891
                                                                 NID:g1001200; PIDN:BAA10470.1; to the EMBL Data Library, June
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      malate dehydrogenase - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 11-Jun-1999
C;Accession: E70453
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C;Superfamily: L~lactate dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE000756; NID:92984076; PIDN:AAC07619.1; PID:92984080; GB:AE00065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA .
A; Residues: 1-335 <AQF>
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Best Local :
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Matches
         237
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                                                                                                                                    122
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                                        239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130
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                                                                                                                                                                                                                                                                                    12 IAMVGSGMIGGTMAFLCSLRELGDVVLFDV-----VPNMPMGKAMDISHNSSVVDTGI
                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75
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les 128; Conserv
T-SAYYAPAAAIVDMIEALVQNSKRILPCSVYLDGEAGEYYGVQGFCVGVPVKLGSNGVE
                             QGSAYYAPGASAIQMAESYLKDRKRVMVCSCYLQGQ----YGVQNHYLGVPCVIGGRGVE
                                                                                 KSYCPNAFVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRD
                                                                                                                                                                                                                      TVYG-----SNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAI 118
                                                                                                                          KRYAPDAIVIVVTNPVDVMTYVAYKLLNFPKNRVMGMAGVLDSARFKTFISEELMVSPKD
                                                                                                                                                                                        RVECYTVTPEGEGYEPLEGSDIVVITAGFPRRPG----MSREDLLEANIRIISVIADRI 121
                                                                                                                                                                                                                                                       VAVIGAGNVGEHVASLILLKNLANVKMFDLPRKTEEKVFEPVKGKALDMKQMLAAMDIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSIDEVK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNPLDVMTYLAWKVTGLPSQRVMGMAGVLDSARLKAFIAMKLGACPSDINTLVLGGHGDL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVIGVHGDH 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIAMVGSGMIGGTMAFLCSLRELGDVVLFDVVPNMFMGKAMDISHNSSVVDTGITVYGSN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IQMAESYLKDRKRVMVCSCYLQGQYGVQNHYLGVPCVIGGRGVGKIIELELTAQERQELQ 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLPLPRYCTVSGVPITEL - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EYEATAGSDVVVITAGLPRRPG-----MSRDDLLGKNANIVAQGAREALRYSPNAILIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAFVINI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVTVVGAGNVGRTLAQRLVQQNVANVVLLDIVPGLPQGIALDLMAAQSVEEYDSKIIGTN
                                                                                                                                                                                                                                                                                                                             132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G.; Warren, P.V.; Gaasterland, T.;
                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                        35.9%;
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                                                                                                                                                                                                                                                                                                                      72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66;
                                                                                                                                                                                                                                                                                                                     Score 605.5; DB 2
Pred. No. 4.7e-39;
2; Mismatches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               · IPPQTIEELVERTRNGGAEIAALLQTGTAYYAPASSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 2.96
56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
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ches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Young,
                                                              -EKLEKIIERTRFGGGEIVNLMG
                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                        104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W.G.;
                                                                                                                                                                                                                                                                                                                                                  Length 335;
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                     31;
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C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: L-lactate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE000750; NID:g2983999; A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A70300; MUID:98196666
A;Accession: D70444
A;Status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
300 FELVNLSGYEKRELLRSAKTLKEM 323
                                                                         241
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                                                                                                                                               186
                                                                                                                                                                   180 QGMVIGVHGDHMVPLSRYATVNGIPLSEFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQ 239
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                                296 IIELELTAQERQELQGSIDEVKEM 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 9 RPKIAMVGSGMIGGTMAFLCSLRELGDVVLF-----DVVPNMPMGKAMDISHNSSVVDTG 63 :|||:::|: | :|: :::|
                                                                                                GSAYYAPGASAIQMAESYLKDRKRVMVCSCYLQGQ----YGVQNHYLGVPCVIGGRGVEK
                                                                                                                                    RTLVLGTHGDLMVPVTSHSFIGDKPIEEV----FSASEIDELIEKTRKGGAQIVSLMGT
                                                                                                                                                                                                                                                                                                         ITV----YGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIK 119
                                                                                                                                                                                                                                                                                                                                             KPKISVIGAGKVGENVAYLLTILGLGDVYLFARYKKGLEP--AKAKALDLKQMAVLMDID
                                                                  -SAYYAPAASVVIMVESIINDRKRVMPCSVYVEGEAAKHYEIEGVCIGLPVVLGKKGVED
                                                                                                                                                                                                     EYAKDSIIIVVSNPVDTLTYATIKLTGFEPRRVIGMAGVLDSARFKNFVKEKIGISNADI
                                                                                                                                                                                                                                       SYCPNAFVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDV
                                                                                                                                                                                                                                                                         INVKGISYDKEGFEELKGSDIVVITAGIPRREG-----MSREDLLYENLKILKKFTDAIK 125
                                                                                                                                                                                                                                                                                                                                                                                                                         121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       33.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                       76;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 569;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN: AAC07547.1;
                                                                                                                                                                                                                                                                                                                                                                                                                     101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:92984002; GB:AE00
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                                                                                                                                  240
                                                                                                  295
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R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K. awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A;Reference number: A72450; MUID:99310339
                                                                                                                                                                                                                                                                                                                          C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision
                               A; Residues:
                                                                                       A:Status: preliminary
                                                           A; Molecule type:
                                                                                                                         A; Accession: E72655
                                                                                                                                                                                                                                                                                                        C; Accession: E72655
                                                                                                                                                                                                                                                                                                                                                                               probable malate dehydrogenase APE0672 - Aeropyrum pernix (strain K1)
references:
                            1-313 <KAW>
                                                                 DNA
                                                                                                                                                                                                                                                                                                                    20-Aug-1999 #text_change 20-Jun-2000
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DDBJ:AP000060; NID:g5104188; PIDN:BAA79645.1; PID:g5104330

strain

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iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Saddie, Y.; Sato, T.; Scanlon A; Authors: Schleich, S.; Schroetter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seronakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, I.; A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A.; Reference number: A69580; MUID:98044033
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                                                                                          Biol. Chem. Hoppe-Seyler 367, 891-903, 1986
Biol. Chem. Hoppe-Seyler 367, 891-903, 1986
A; Title: Structure and function of L-lactate dehydrogenases
A; Reference number: A25805; MUID:87076052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo; V.; C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferra
                                                                                                                                                                                        A; Experimental source: strain 168 R; Hediger, M.A.; Frank, G.; Zuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D. Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision
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                                                                                  A; Accession:
                                                                                                                                                                                                                                                                           A; Residues: 1-321 <KUN>
                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                          A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: E69649; A25805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus subtilis
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C; Superfamily:
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                                                                                                                                                                                                                                   Cross-references: GB:299105; GB:AL009126; NID:g2632457; PIDN:CAB12099.1; PID:g2632591
;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 GLVLTVEAIKRDSKRIYPYSLYLQGEYGYNDIVAEVPAVIGKSGIERIIELPLTEDEKRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 FDEAVQAVKKLVETL 307
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                                                                                                                                                                                                                                                                                                                                                          E69649
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                         ,40-51,'N',53-57,'AP',60-120,'I',122-224,'T',226-315,'VN'
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                                                                                                                                                                                     Zuber,
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Pred. No. 1.2e-35;
'2; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEIEEVVSETVNAGAKITELRGY-SSNYGPAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #text_change 20-Jun-2000
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                                                                                                                               from thermophilic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.; Sekowska, A.; Seroj
.; Tosato, V.; Uchiyama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.; Galizzi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Carter, N.M.; Ch
, C.; Ferrari, E.
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Query Match Best Local

Similarity

27.0%;

Score 455; Pred. No. 1

.5e-DB 1;

Length 318

Indels

16;

Mismatches

Conservative

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A;Description: catalyzes the reversible oxidation of (S)-lacta C;Superfamily: L-lactate dehydrogenase C;Keywords: homotetramer; NAD; oxidoreductase F;1-318/Product: L-lactate dehydrogenase #status experimental F;11-41/Region: beta-alpha-beta NAD nucleotide-binding fold
                                                                                                                                                     C; Function:
                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 1-318 <STA>
                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:M22305; NID:g143135; PIDN:AAA22566.1; PID:g143136
R;Stangl, D.; Wiederkehr, F.; Suter, F.; Zuber, H.
Biol. Chem. Hoppe-Seyler 368, 1157-1166, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Structure and function of L-lactate dehydrogenases from thermophilic and megaterium. Preparation and properties of a hybrid lactate dehydrogenase compris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Waldvogel, S.: Weber, H.: Zuber, H. Biol. Chem. Hoppe-Seyler 368, 1391-1399,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Bacillus megaterium C;Date: 03-Aug-1984 #sequence_revision
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F;154,181/Active site: Asp, His
                                                                                                                                                                                                                                                  A;Reference number: S01472; MUID:88050100 A;Accession: S01472
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                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-318 <W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: S00133; MUID:88107005
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                                                                                                                                                                  ;Comment: This enzyme is activated by fructose-1,6-diphosphate
                                                                                                                                                                                                                                                                                                                          ;Title: Structure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 EKEQFLHSAGVLKNILK 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 VHGDHMVPLSRYATVNGIPLSEFVKKG-WIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 IFLVATNPVDILTYATWKFSGLPKERVIGSGTTLDSARFREMLSEYFGAAPQNVHAHIIG
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106; Conser
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  #status predicted
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Pred. No. 6.2e-28;
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L-lactate dehydrogenase (EC 1.1.1.27) - Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_chan
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C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 22-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 18-Jun-1999
C;Accession: S36683; S36864; D72202
R;Ostendorp, R; Liebl, W; Schurig, H.; Jaenicke, R.
Eur. J. Biochem. 216, 709-715, 1993
A;Title: The L-lactate dehydrogenase of the hyperthermophilic bacterium Thermotoga
                       R;Fraser, C.M.; Gocayne, J.D.; White, O.; M.; Fuhrmann, J.; Nguyen, D.; Utterback, '
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A;Residues: 1-31,38-53,55-85,163-173 <0S2>
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.;
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richards
                                                                     C; Accession: H64250
                                                                                                                                                                  H64250
                                                                                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A72200;
A;Accession: D72202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-319 <OST>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Status: preliminary
;Molecule type: DNA
;Residues: 1-319 <ARN>
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Best Local Similarity 33.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: GB:AE001823; GB:AE000512; NID:g4982441; PID:g4982452; TIGR:TM1867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Gene: TM1867
  C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: L-lactate dehydrogenase
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Fuhrmann, J.; Nguyen, A.; Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                 231
                                                                                                                                                                                                                                                                                                                                                                                                                                              175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 ITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVIGVHGD 189
                                                                                                                                                                                                                                                           291
                                                                                                                                                                                                                                                                                                                                                                                  247 GASAIQMAESYLKDRKRVMVCSCYLQGQYGVQNHYLGVPCVIGGRGVEKIIELELTAQER 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 HMVPLSRYATVNGIPLS---EFVKKGWIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYYAP 246
                                                                                                                                                                                                                                                                                                 307 QELQGSIDEVKEMQKAIAA 325
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                                                                                                                                                                                                                                                                                                                                       ALAVADIVESIFFDEKRVLTLSVYLEDYLGVKDLCISVPVTLGKHGVERILELNLNEEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                SEVPVWSGAMIGGIPLQNMCQICQK--CDSKILENFAEKTKRAAYEIIE--RKGATHYAI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIGIVGLGRVGSSTAFALLMKGFAREMVLIDVDKKRAEGDALDLIHGTPFTRRA-NIY-A 59
                                                                                                                                                                                                                                                        EAFRKSASILKNAINEITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lateral gene transfer between Archaea and Bacteria 72200; MUID:99287316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.0%;
                   J.D.; White, O.; Adams, M.D.; Clayton, D.; Utterback, T.R.; Saudek, D.M.; Ph
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                                                                                                                                                                                                                                                      309
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                                                                                   17-Nov-1995 #text_change
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              on, R.A.; Fleischmann, Phillips, C.A.; Merri
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A;Experimental source: strain ATCC393
R;Hensel, R; Mayr, U.; Yang, C.
Eur. J. Biochem. 134, 503-511, 1983
A;Title: The complete primary structure of the allosteric L-lactate dehydrogenase fro A;Reference number: A00352; MUID:83287369
A;Accession: A00352
                                                                                                                                                                                                                 submitted to JIPID, November 1991
A;Reference number: JU0280
A;Accession: JU0280
                                                                                                                                                                                                                                                                                                                                                                                  R;Kim, S.F.; Baek, S.J.; Pack, M.Y.
Appl. Environ. Microbiol. 57, 2413-2417, 1991
A;Title: Cloning and nucleotide sequence of tl
A;Reference number: A43944; MUID:92117575
A;Accession: A43944
A;Molecule type: protein
A;Residues: 2-25,'f','27-51,'T',53-87,'KQ',90-118,'L',120-269,'I',271-272,'L',274-326
                                                                                                                                                                               A; Residues:
                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                               R;Taguchi, H.;
                                                                                                                                                                                                                                                                                                 A; Experimental source: strain ATCC 39
A; Note: sequence extracted from NCBI
                                                                                                                                                                                                                                                                                                                                                A; Residues: 1
                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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C;Keywords: oxidoreductase
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C;Species: Lactobacillus casei
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A; Residues: 1-312 <TIGR>
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A; Title: The minimal gene
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 INITAPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVIGVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAFV 127
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                                                                                                                                                                               2-326 <TAG>
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ce: strain G-37
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BI backbone
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                                                                                                                                                                                                                                                     C;Superfamily: L-lactate dehydrogenase
C;Reywords: homotetramer; NAD; oxidoreductase
F;1-319/Product: L-lactate dehydrogenase X #status
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C;Superfamily: L-lactate dehydrogenase
C;Reywords: homotetramer; NAD; oxidoreductase
F;2-326/Product: L-lactate dehydrogenase #status experimental <MAT>
F;11-41/Region: beta-alpha-beta NAD nucleotide-binding fold
F;154,181/Active site: Asp, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A:Gene: l-lct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              v.Title: Structure and function of L-lactate dehydrogenases use genes of the psychrophilic bacterium Bacillus psychrosac
                                                                                                                                                                                                                                                                                                                                                                                           Residues: 1-319 <V
                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vckovski, V.; Schlatter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·lactate dehydrogenase (EC 1.1.1.27) X - Bacillus psychrosaccharolyticus Species: Bacillus psychrosaccharolyticus
                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                             Molecule type: protein Residues: 1-24 <SCH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: S08183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reference number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date: 30-Jun-1991 #sequence_revision 30-Jun-1991
                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                       Accession: A38031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 QGMVIGVHGDHMVPLSRYATVNGIPLSEFVK-KGWIKQEEVDDIVQKTKVAGGEIVRLLG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 DSGFNGIFLVAANPVDILTYATWKLSGFPKNRVVGSGTSLDTARFRQSIAEMVNVDARSV 173
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                                                                                                  11 KIAMVGSGMIGGTMAFLC---SLRELGDVVLEDVVPNMPMGKAMDISHNSSVVDTGI-TV
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YGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMRE-VGAAIKSYCPNA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAVFEKNTRPKIAMVGSGMIGGTMAFLCSLRELG-DVVLFDVVPNMPMGKAMDISHNSSV 59
                                                          RVALIGAGSVGSSYAFALLNOSITE--ELVIIDVNEDKAMGDAMDLNHGKIFAPNPTKTW 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGATFYGIATALARISKAILNDENAVLPLSVYMDGQYGLNDIYIGTPAVINRNGIQNILE 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGSAYYAPGASAIQMAESYLKDRKRVMVCSCYLQGQYGVQNHYLGVPCVIGGRGVEKIIE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTSPKKIY-SAEYSDAKDADLVVITAGAPQKPGE----TRLDLVNKNLKILKSIVDPIV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VDTGITVYGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MASITDKDHQKVILVGDGAVGSSYAYAMVLQGTAQEIGIVDIFKDKTKGDAIDLS-NALP 59
                                                                                                                                                                                                                                                                                                                                                                                           1-319 <VCK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoppe-Seyler 371,
                                                                                                                                                                            Similarity
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                                                                                                                                                     Conservative
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29.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUID: 90241471
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                                                                                                                                                     76;
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                                                                                                                                                                     Score 431; DB 2
Pred. No. 1e-25;
                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1990
                                                                                                                                                                                       DB 2;
                                                                                                                                                 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              psychrosaccharolyticus
                                                                                                                                                                                                                                                          experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #text_change 14-May-1993
                                                                                                                                                                                         Length 319;
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29,6
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                                                                                                                                                                                                                                                      66 YG--NYDDCKEADIVCICAGANQKPGE----TRLDLVEKNLKIFKSLVDQVMASGFDGI
                             ERQELQGSIDEVKEM 319
                                                                                      APGASAIQMAESYLKDRKRVMVCSCYLQGQYGVQNHYLGVPCVIGGRGVEKIIELELTAQ
                                                                                                                                                                                    FLI-ATNPVDILTYATWKFSGLPKERVIGSGTILDSGRFRFLLGEYFDIAPANVHAHIIG
                                                                                                                                                                                                                    FVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVSPRDVQGMVIG
EQKQFTHSSTVLKEI 310
                                                           GIAMGLARITKAILNNENSVLTVSTYLDGEYGEKDVYIGVPAVVNRTGIREILELTLSET 295
                                                                                                                        EHGDTELPVWSHADIGGVPVEELITRNPEYKMEDLDQLFVNVRDAAYHIIK--KKGATYY
                                                                                                                                                      VHGDHMVPLSRYATVNGIPLSEFVKKG-WIKQEEVDDIVQKTKVAGGEIVRLLGQGSAYY
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